- ProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis
 4922 CCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC
 GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGAGGTG

4954 NCOI,

4893 BGL2,

SerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro 4982 AGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGTACCG TCAATGAGAGGTCCACTTTAGTTATCCCACCGGCGTACGGAGTCTTTTGAACCCCATGGC

5015 SPHI, 5035 KPNI,

ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly
5042 CCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCAGGCTTCTGGCCAGAGGA
GGGAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGCGATCCGAAGACCGGTCTCCT

5064 APAI, 5091 BALI,

GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys 5102 GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAAA CCGTCCCGACGGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCGAGTTT

5113 NDEI,

5174 NOTI, 5175 EAG1 XMA3, 5182 BALI, 5186 PVU2,

SerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys
5222 AGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCCGCTGGATCTGGTTTTGC
TCGCCCCCTCTGTAAATAGTGTCGCACAGAGTACGGGCCGGGCGACCTAGACCAAAACG

5240 DRA3,

LeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgMetSerThrAsn
5282 CTACTCCTGCTGCAGGGGTAGGCATCTACCTCCTCCCCAACCGAATGAGCACGAAT
GATGAGGACGACGACGTCCCCATCCGTAGATGAGGAGGGGTTGGCTTACTCGTGCTTA

5295 PSTI,

ProLysProGlnArgLysThrLysArgAsnThrAsnArgArgProGlnAspValLysPhe
5342 CCTAAACCTCAAAGAAAGACCAAACGTAACACCAACCGGCGCCGCGGGCCGAGGTCAAGTTC
GGATTTGGAGTTCTTCTGGTTTGCATTGTGGTTGGCCGCCGGCGTCCTGCAGTTCAAG

5380 NOTI, 5381 EAG1 XMA3, 5390 AAT2, 5401 SMAI XMAI,

ProGlyGlyGlnIleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeu
5402 CCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCTAGATTG
GGCCCACCGCCAGTCTAGCAACCACCTCAAATGAACAACGGCGCGTCCCCGGGATCTAAC

4229 DRD1, 4236 ALWN1,

TECH CENTER 1600/2900

- GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer
 4262 GAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAAGTCC
 CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCGCACCGGTAGTTCAGG
 - 4301 BGLI, 4308 BALI,
- LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
 4322 CTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGCGGC
 GAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCTCTTGACGCCG
 - 4345 APAI,
- TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys
 4382 TATCGCAGGTGCCGCGCGAGCGGCGTACTGACAACTAGCTGTGGTAACACCCTCACTTGC
 ATAGCGTCCACGGCGCGCTCGCCGCATGACTGTTGATCGACACCATTGTGGGAGTGAACG
- TyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuVal
 4442 TACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCTCGTG
 ATGTAGTTCCGGGCCCGTCGGACAGCTCGGCGTCCCGAGGTCCTGACGTGCTACGAGCAC
 - 4452 SMAI XMAI,
- CysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
 4502 TGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGCGAGC
 ACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGCCGCTCG
 - 4508 DRD1, 4511 TTH3I,
- LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln
 4562 CTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCTGGGGACCCCCACAA
 GACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGGACCCCTGGGGGGTGTT
- ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp
 4622 CCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCACGAC
 GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTGCTG
 - 4637 SACI,
- GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla
 4682 GGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGCGAGAGCT
 CCGCGACCTTTCTCCCAGATGATGGAGTGGGCACTTGGGATGTTGGGGGGAGCGCTCTCGA
 - 4731 NRUI,
- AlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe
 4742 GCGTGGGAGACAGCAAGACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT
 CGCACCCTCTGTCGTTCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTACAAA
- AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla 4802 GCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCC CGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAATATCGG
 - 4806 PFLM1, 4807 DRA3,
 - ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu

	^
	3589 DRA3, 3600 SAC2,
3602	AlaGluGluGlnLysLeuProlleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsn GCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCACCACAAT CGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTGGTGTTA
	3611 ALWN1, 3655 PFLM1,
3662	LeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAsp TTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACATTTGAC AACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGTAAACTG
	3681 DRA3,
3722	ArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAlaAGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAGCGGCGTCTGACGTTCAAGACCTGCCGCCGCTCTGACGTTCAAGACCTGCCGCTAATGGTCCTGCATGAGTTCCTCCAATTTCGTCGCCGC
3782	SerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProProHis TCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCCACAC AGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGGTGTG
	3816 HIND3,
3842	SerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAla TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAAGGCC AGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTCCGG
	3875 AAT2, 3890 BGLI,
3902	ValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIleAsp GTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAATAGAC CATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTATCTG
3962	ThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys ACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGTCGTAAG TGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCAGCATTC
4022	ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu CCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATGGCTTTG GGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTACCGAAAC
4082	TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr TACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCAATAC ATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAGGTTATG
4142	SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet TCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCCAATG AGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGGGGTTAC

GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr 4202 GGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACG CCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCACTCGCTGTAGGCATGC

4160 ECORI,

- ThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln 2942 ACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAG TGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTC 2966 ESP1, 2969 SACI, GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer 3002 GAGATGGCCGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCC CTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTGAGG PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu 3062 TTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAAATCCTG AAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGAC 3096 BGL2, ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro 3122 CGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAACCCC GCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGCCAAACCCGCGCCGGCCTGATATTGGGG 3143 ALWN1, 3164 EAG1 XMA3, ProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysPro 3182 CCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTGCCCG GGCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCGACGGGC 3217 HGIE2, 3229 NCOI, LeuProProProLysSerProProValProProProArgLysLysArgThrValValLeu CTTCCACCTCCAAAGTCCCCTCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTGGTCCTC GAAGGTGGAGGTTTCAGGGGAGGACACGGAGGCGGAGCCTTCTTCGCCTGCCACCAGGAG ThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSer 3302 ACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAGCTCC TGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCGTCGAGG 3332 SACI, 3346 HIND3, SerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGly CysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluPro 3422 TGCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCTGGAGGGGGAGCCT ACGGGGGGGCTGAGGCTCAGGATAAGGAGGTACGGGGGGGACCTCCCCTCGGA 3437 EAM11051. GlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGlu GGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAACGCGGAG CCCCTAGGCCTAGAATCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTGCGCCTC 3484 BAMHI, 3485 BSAB1, 3487 BSPE1, AspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAla
 - FIG. 22-Page 6

GATGTCGTGTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTGCGCC CTACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCACGCGG 3589 DRA3, 3600 SAC2,

AlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsn
GCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCACCACAAT
CGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTGGTGTTA

3611 ALWN1, 3655 PFLM1,

LeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAsp 3662 TTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACATTTGAC AACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGTAAACTG

3681 DRA3,

- ArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAla
 3722 AGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAGCGGCG
 TCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTTCGTCGCCGC
- SerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProProHis
 TCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCACAC
 AGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGGTGTG

3816 HIND3.

SerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAla
TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAAGGCC
AGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTCCGG

3875 AAT2, 3890 BGLI,

- ValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIleAsp
 3902 GTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAATAGAC
 CATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTATCTG
- ThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys
 3962 ACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGGTCGTAAG
 TGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCAGCATTC
- ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu CCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATGGCTTTG GGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTACCGAAAC
- TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr
 4082 TACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCAATAC
 ATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAGGTTATG
- SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet 4142 TCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCCAATG AGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGGGGTTAC

4160 ECORI,

GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr 4202 GGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACG CCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAGGCATGC

- LysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle 2342 AAGGGGTCTGGCGAGGGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGAGATC TTCCCCCAGACCGCTCCCCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAG ThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArgThrCysArgAsnMet ACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGGAACATG TGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGCCAGGATCCTGGACGTCCTTGTAC 2425 BSAB1, 2441 AVR2, 2448 SSE83871, 2449 PSTI, ${\tt TrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAla}$ 2462 TGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTTCCTGCG ACCTCACCCTGGAAGGGGTAATTACGGATGTGGTGCCCGGGGACATGGGGGGAAGGACGC 2480 ASE1, 2497 APAI, ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln 2522 CCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAG GGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTATTCCGTC 2553 PSTI. ${\tt ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln}$ 2582 GTGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG CACCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGTC 2594 DRA3, ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro 2642 GTCCCATCGCCCGAATTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCC CAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGG ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro 2702 CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATACCCG GGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGC 2757 HGIE2. ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu 2762 GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCATGCTC CATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTACGAG 2809 AAT2, ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerPro 2822 ACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATCACCC TGACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCCGCTTCCAACCGCTCCCCTAGTGGG 2850 EAG1 XMA3, ${\tt ProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys}$
 - FIG. 22-Page 5

CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG

2889 BALI, 2903 NHEI,

1742	ValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeuAlaGTGGCTGCCCAGCTCGCCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGCTTAGCTCACCGACGGGTCGAGCGGGGGCCGAATCGACGGAAACACCCGCGACCGAATCGA
	1794 ESP1,
1802	GlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGlyTyr GGCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGACATCCTTGCAGGGTAT CCGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGTCCCATA
	1802 KAS1 NARI,
1862	GlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValProSer GGCGCGGGCGTGGCGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCCCTCC CCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGGAGG
	1878 SACI, 1899 BSPH1,
1922	ThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGlyACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTCGGCTGCCTCCTCGCAGCCATCCTCCTCGGAGCCATCAGCCGAGCCTCGGGAGCATCAGCCGAGCCTCCGGAGCATCAGCCGAGCCTCGGAGCATCAGCCGAGCCTCGGAGCATCAGCCGAGCCTCGGAGCATCAGCCGAGCCTCGGAGCATCAGCCGAGCCTCGGAGCATCAGCCGAGCCTCGGAGCATCAGCCGAGCCTCGGAGCATCAGCCGAGCCTCGGAGCATCAGCCGAGCCTCGGAGCATCAGCCGAGCCTCGGAGCATCAGCCGAGCCTCGGAGCATCAGCCGAGCCTCGGAGCATCAGCCGAGCCTCGGAGCATCAGCCGAGCCTCGGAGCATCAGCCGAGCCCGAGCCTCGGAGCCATCAGCCGAGCCCGAGCCCTCGGAGCCATCAGCCGAGCCGGAGCCCTCGGAGCCATCAGCCGAGCCCGAGCCCTCGGAGCCATCAGCCGAGCCCGAGCCCTCGGAGCCATCAGCCGAGCCCGAGCCCCGAGCCCCGAGCCCCCGAGCCCCCGGAGCCCCCAGCCCCGCCATCCAGCCCGAGCCCCCCAGCCCCATCCCCCGGAGCCCCCCGCCATCCCCCGCAGCCCCCCGCCCCCCCC
	1928 TTH3I,
1982	ValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrp GTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTGCAGTGG CACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCCCGTCACGTCACC
	2004 NAEI, 2017 SMAI XMAI,
2042	MetAsnArgLeulleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrVal ATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCACTACGTG TACTTGGCCGACTATCGGAAGCGGAGGCCCCCCTTGGTACAAAGGGGGTGCGTGATGCAC
	2067 SMAI XMAI, 2093 DRA3,
2102	ProGluSerAspAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGln CCGGAGAGCGATGCAGCTGCCGGGTCACTGCCATACTCAGCAGCCTCACTGTAACCCAG GGCCTCTCGCTACGTCGACGGGCGCAGTGACGGTATGAGTCGTCGGAGTGACATTGGGTC
	2115 PVU2, 2159 ALWN1,
2162	LeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer CTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGGTTCC GAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGGCCAAGG
	2164 MST2, 2220 ECON1,
2222	TrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu TGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGGCTA ACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACTCGCTGAAATTCTGGACCGAT
2282	LysAlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArgGlyTyr AAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCTTTGTGTCCTGCCAGCGCGGGTAT TTTCGATTCGA
	2285 ESP1, 2300 PVU2, 2310 BAMHI,

 ${\tt ThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln}$ ACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAG TGGCGATTGGTACTGAGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTC 2966 ESP1, 2969 SACI, GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer 3002 GAGATGGGCGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCC CTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTGAGG PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu 3062 AAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGAC 3096 BGL2. ${\tt ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro}$ 3122 CGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAACCCC GCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAAACCCGCGCCGGCCTGATATTGGGG 3143 ALWN1, 3164 EAG1 XMA3, ProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysPro 3182 CCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTGCCCG GGCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCGACGGGC 3217 HGIE2, 3229 NCOI, LeuProProProLysSerProProValProProProArgLysLysArgThrValValLeu 3242 CTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTGGTCCTC GAAGGTGGAGGTTTCAGGGGGGGGAGCACGGAGCCTTCTTCGCCTGCCACCAGGAG Thr Glu Ser Thr Leu Ser Thr Ala Leu Ala Glu Leu Ala Thr Arg Ser Phe Gly Ser Ser3302 ACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAGCTCC TGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCGTCGAGG 3332 SACI, 3346 HIND3, SerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGly 3362 CysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluPro ACGGGGGGGCTGAGGCTCAGGATAAGGAGGTACGGGGGGGACCTCCCCTCGGA 3437 EAM11051. ${\tt GlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGlu}$ GGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAACGCGGAG CCCCTAGGCCTAGAATCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTGCGCCTC 3484 BAMHI, 3485 BSAB1, 3487 BSPE1, AspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAla GATGTCGTGTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTGCGCC 3542

CTACAGCACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCACGCGG

LysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle 2342 AAGGGGTCTGGCGAGGGGACGCATCATGCACACTCGCTGCCACTGTGGAGCTGAGATC TTCCCCCAGACCGCTCCCCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAG $Thr Gly {\tt His Val Lys As n Gly Thr Met Arg Ile Val Gly Pro Arg Thr Cys Arg As n Met Thr Gly {\tt His Val Lys As n Gly Thr Met Arg Ile Val Gly Pro Arg Thr Cys Arg As n Met Thr Gly {\tt His Val Lys As n Gly Thr Met Arg Ile Val Gly Pro Arg Thr Cys Arg As n Met Thr Gly {\tt His Val Lys As n Gly Thr Met Arg Ile Val Gly Pro Arg Thr Cys Arg As n Met Thr Gly {\tt His Val Lys As n Gly Thr Met Arg Ile Val Gly Pro Arg Thr Cys Arg As n Met Thr Gly {\tt His Val Lys As n Gly Thr Met Arg Ile Val Gly Pro Arg Thr Cys Arg As n Met Thr Gly {\tt His Val Lys As n Gly Thr Met Arg Ile Val Gly Pro Arg Thr Cys Arg As n Met Thr Gly {\tt His Val Lys As n Gly Thr Met Arg Ile Val Gly Pro Arg Thr Cys Arg As n Met Thr Gly {\tt His Val Lys As n Gly Thr Met Arg Ile Val Gly Pro Arg Thr Cys Arg As n Met Thr Gly {\tt His Val Lys As n Gly Thr Met Arg Ile Val Gly Pro Arg Thr Cys Arg As n Met Thr Gly {\tt His Val Lys As n Gly Thr Met Arg Ile Val Gly Pro Arg Thr Cys Arg As n Met Thr Gly {\tt His Val Lys As n Gly Thr Met Arg Ile Val Gly Pro Arg Thr Gly {\tt His Val Lys As n Gly Thr Met Arg Ile Val Gly {\tt His Val Lys As n Gly Thr Met Arg Ile Val Gly {\tt His Val Lys As n Gly Thr Met Arg Ile Val Gly {\tt His Val Lys As n Gly Thr Met Arg Ile Val Gly {\tt His Val Lys As n Gly {\tt His Val Lys {\tt His Val$ 2402 ACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGGAACATG TGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGCCAGGATCCTGGACGTCCTTGTAC 2425 BSAB1, 2441 AVR2, 2448 SSE83871, 2449 PSTI, TrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAla 2462 TGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTTCCTGCG ACCTCACCCTGGAAGGGGTAATTACGGATGTGGTGCCCGGGGACATGGGGGGAAGGACGC 2480 ASE1, 2497 APAI, ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln 2522 CCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAG GGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTATTCCGTC 2553 PSTI, ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln 2582 GTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG CACCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGTC 2594 DRA3. ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro 2642 GTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCC CAGGGTAGCGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGG ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTvrPro 2702 CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATACCCG GGGACGTTCGGGAACGACGCCCTCCTCATAGTAAGTCTCATCCTGAGGTGCTTATGGGC 2757 HGIE2, ${\tt ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu}$ 2762 GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCATGCTC CATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTACGAG 2809 AAT2, ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerPro 2822 ACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATCACCC TGACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCCGCTTCCAACCGCTCCCCTAGTGGG 2850 EAG1 XMA3, ProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG 2889 BALI, 2903 NHEI,

1742	ValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeuAlaGTGGCTGCCCAGCTCGCCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGCTTAGCCCACCGACCG
	1794 ESP1,
1802	GlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGlyTyr GGCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGACATCCTTGCAGGGTAT CCGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGTCCCATA
	1802 KAS1 NARI,
1862	GlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValProSer GGCGCGGGCGTGGCGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCCCTCC CCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGGAGG
	1878 SACI, 1899 BSPH1,
1922	ThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGlyACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTCGGCTGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCATCAGCCG
	1928 TTH3I,
1982	ValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrp GTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTGCAGTGG CACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCCCGTCACGTCACC
	2004 NAEI, 2017 SMAI XMAI,
2042	MetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrVal ATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCCACGCACTACGTG TACTTGGCCGACTATCGGAAGCGGAGGCCCCCTTGGTACAAAGGGGGTGCGTGATGCAC
	2067 SMAI XMAI, 2093 DRA3,
2102	ProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGln CCGGAGAGCGATGCAGCTGCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAACCCAG GGCCTCTCGCTACGTCGACGGCGCGCAGTGACGTTATGAGTCGTCGGAGTGACATTGGGTC
	2115 PVU2, 2159 ALWN1,
2162	LeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer CTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGGTTCC GAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGGCCAAGG
	2164 MST2, 2220 ECON1,
2222	TrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu TGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGGCTA ACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACTCGCTGAAATTCTGGACCGAT
2282	LysAlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArgGlyTyr AAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCTTTGTGTCCTGCCAGCGCGGGTAT TTTCGATTCGA

2285 ESP1, 2300 PVU2, 2310 BAMHI,

TCCCGAGTTCGGGG	AGGGGGTAGCACCCTGGTCT	TACACCTTCACAAACTAAGCGGAG	ኮጥረ
	AGGGGG LAGCACCC LGG LC	IMCACCITICACAAACIAAMGCCGCGAG	1

- ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle
 1142 CCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAAATC
 GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAG

 1150 NCOI.
- ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu
 1262 GTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTATTGCCTG
 CAGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGACGAAACCGGCGCATAACGGAC
- SerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIleIle
 1322 TCAACAGGCTGCGTGGTCATAGTGGGCAGGCTCGTCTTGTCCGGGAAGCCGGCAATCATA
 AGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGTTAGTAT

1369 NAEI,

- ProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeu
 1382 CCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTA
 GGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACCTTCTCACGAGAGTCGTGAAT

 1385 DRD1,
- ProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeu 1442 CCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTC GGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAGCCGGAG
- LeuGlnThrAlaSerArgGlnAlaGluVallleAlaProAlaValGlnThrAsnTrpGln
 1502 CTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAACTGGCAA
 GACGTCTGGCGCAGGCCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTGACCGTT

 1502 PSTI, 1507 TTH31,
- LysLeuGluThrPheTrpAlaLysHisMetTrpAsnPhelleSerGlylleGlnTyrLeu
 1562 AAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATACTTG
 TTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTTATGAAC

 1565 XHOI, 1586 NDEI,
- AlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAla GCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGCT CGCCCGAACAGTTGCGACCATTGGGGCGGTAACGAAGTAACTACCGAAAATGTCGA

1643 BSTE2, 1677 ALWN1 PVU2,

AlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrp
1682 GCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGGGGGTGG
CGACAGTGGTCGGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCCCCCACC

- SerLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaVal
 TCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGCCGTG
 AGTTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACGGCAC
- AlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValValVal

 GCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGTCGTG
 CGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGCTACAACAGCAGCAC

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550 SAC2, 560 DRD1,

AlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerVallleAspCysAsn 602 GCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTGCAAT CGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTA

615 BSPH1,

- ThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIle
 662 ACGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTTCACCATTGAGACAATC
 TGCACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTCTGTTAG
- ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys
 ACGCTCCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGCCAGGGGGAAG
 TGCGAGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCCCCCTTC
- ProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSer
 782 CCAGGCATCTACAGATTTGTGGCACCGGGGGGGGGCCCCCTCCGGCATGTTCGACTCGTCC
 GGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTGAGCAGG

816 BGLI, 833 DRD1,

881 SACI,

ThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu

ACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCATCTT

TGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTGGTAGAA

931 SMAI XMAI.

GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln GAATTTTGGGAGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCCAG CTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTC

985 STUI,

ThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAla
1022 ACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCT
TGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCACACGCGA

1069 DRA3,

ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys
AGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCTCAAG

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1	L	U	_ \	31	U		11	_(36	ď	٠.	Мι	یاو	ىاد	ю	۰	17	ч.	•	:Α	c	C	C	ľ	اوا	G.	Т		ľ	١L	. А	ľ	•	T'	Т	_,	١C	Α	A)	40		Α	А			-	Δ	C'	T٦	rc

- ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle
 1142 CCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAAATC
 GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAG

 1150 NCOI,
- ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu
 1262 GTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTTGGCCGCGTATTGCCTG
 CAGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGACGAAACCGGCGCATAACGGAC
- SerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIleIle
 1322 TCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAATCATA
 AGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGTTAGTAT

 1369 NAEI,
- ProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeu
 1382 CCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTA
 GGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACCTTCTCACGAGAGTCGTGAAT

 1385 DRD1,
- ProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeu
 1442 CCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTC
 GGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAGCCGGAG
- LeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGln
 1502 CTGCAGACCGCGTCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAACTGGCAA
 GACGTCTGGCGCAGGCCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTGACCGTT

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 1502 PSTI, 1507 TTH3I,
- LysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyrLeu
 1562 AAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATACTTG
 TTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTTATGAAC

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 1565 XHOI, 1586 NDEI,
- AlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAla GCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGCT CGCCCGAACAGTTGCGACCGACCATTGGGGCGGTAACGAAGTAACTACCGAAAATGTCGA
 - 1643 BSTE2, 1677 ALWN1 PVU2,
- AlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrp
 1682 GCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGGGGGTGG
 CGACAGTGGTCGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCCCCCACC

TCTGLCGTTCAAGLCTGTCCCT& かっここっしゃ スーカース スーカー・スーカー アーフィー・スーカー アーフィー・スーカー アーフィー・スーカー アーフィー・スーカー アーフィー・スーカー アーフィー・スーカー アーフィー・スーカー アーフィー・スーカー アーフィー・スーカー アーフィー・スープ アーフィー・スールー・スープ アーフィー・スープ アース アーフィー・スープ アーフィー・スー アーフィー・スープ アーフィー・スールー・スープ アーフィー・スープ アーフィー・スープ アース アーフィー・スープ アーフィー・スープ アーフィー・スープ アース アース アーフィー・スープ アース アース アース アース アース アース アース アース アース アース	8 ヤヤヤ にこてにここ	<u>ゃんへゃんへゃんへみ ずに みにずずんしずんべみ き</u>	でらなこらででこれるらなここでこのこのである。
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- SerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProProHis
 TCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCCACAC
 AGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGGTGTG

 3816 HIND3.
- SerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAla
 TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAAGGCC
 AGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTCCGG

3875 AAT2, 3890 BGLI.

- ValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIleAsp
 3902 GTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAATAGAC
 CATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTATCTG
- ThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys
 3962 ACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGGTCGTAAG
 TGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCAGCATTC
- ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu
 4022 CCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATGGCTTTG
 GGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTACCGAAAC
- TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr
 4082 TACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCAATAC
 ATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAGGTTATG
- SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet
 TCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCCAATG
 AGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGGGGTTAC

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 4160 ECORI,
- GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr 4202 GGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACG CCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAGGCATGC

4229 DRD1, 4236 ALWN1,

GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer
4262 GAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAAGTCC
CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCGCACCGGTAGTTCAGG

4301 BGLI, 4308 BALI,

LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
4322 CTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGCGGC
GAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCTCTTGACGCCG

4345 APAI,

- SerLysLysCysAspGluLéuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaVal
 TCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGCCGTG
 AGTTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACGGCAC
- AlaTyrTyrArgGlyLeuAspValSerVallleProThrSerGlyAspValValValVal 542 GCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGTCGTG CGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGCTACAACAGCAGCAC 550 SAC2, 560 DRD1.
- AlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerVallleAspCysAsn
 GCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTGCAAT
 CGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTA

 615 BSPH1.
- ThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIle
 662 ACGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTTCACCATTGAGACAATC
 TGCACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTCTGTTAG
- ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys
 ACGCTCCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGGGAAG
 TGCGAGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCCCCCTTC
- ProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSer
 CCAGGCATCTACAGATTTGTGGCACCGGGGGGGGGCCCCCTCCGGCATGTTCGACTCGTCC
 GGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTGAGCAGG
 - 816 BGLI, 833 DRD1,
- - 881 SACI.
- ThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu
 902 ACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCATCTT
 TGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTGGTAGAA
 - 931 SMAI XMAI.
- GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln GAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCCAG CTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTC
 - 985 STUI,
- ThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAla
 1022 ACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCT
 TGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCACACGCGA
 - 1069 DRA3.
- ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys AGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCTCAAG

2		CAAAACAAAAT	GGCTGCATATO	AlaAlaGlnGlyTyrLysValLeuValLeuAsr GCAGCTCAGGGCTATAAGGTGCTAGTACTCAAC CGTCGAGTCCCGATATTCCACGATCATGAGTTC
	^		^	^
	1 HIND3	, 24 NDEI,	52 SCAI.	

ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAsp 62 CCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATCGAT GGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTAGCTA

116 CLAI,

- ProAsnileArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThr
 122 CCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTCCACC
 GGATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAGGTGG
- TyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCys
 TACGGCAAGTTCCTTGCCGACGGCGGTGCTCGGGGGGGCGCTTATGACATAATAATTTGT
 ATGCCGTTCAAGGAACGGCTGCCGCCACGAGCCCCCCGCGAATACTGTATTATTAAACA
- AspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGln
 GACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCACTGTCCTTGACCAA
 CTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAACCGTGACAGGAACTGGTT
- AlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySerVal
 GCAGAGACTGCGGGGGGGGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTCCGTC
 CGTCTCTGACGCCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCCGAGGCAG

 303 ALWN1,
- ThrValProHisProAsnileGluGluValAlaLeuSerThrThrGlyGluIleProPhe
 ACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCTTTT
 TGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAGGGAAAA
- TyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHis
 TACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTGTCAT
 ATGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCCTCTGTAGAGTAGAAGACAGTA

FIG. 22-Page 1

5449 APAI,

- GlyValArgAlaThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnPro
 5462 GGTGTGCGCGACGAGAAAGACTTCCGAGCGTCGCAACCTCGAGGTAGACGTCAGCCT
 CCACACGCGCGCTGCTCTTTCTGAAGGCTCGCCAGCGTTGGAGCTCCATCTGCAGTCGGA
 - 5467 BSSH2, 5478 XMNI, 5502 XHOI, 5511 AAT2,
- IleProLysAlaArgArgProGluGlyArgThrTrpAlaGlnProGlyTyrProTrpPro
 5522 ATCCCAAGGCTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGGCCC
 TAGGGGTTCCGAGCAGCCGGGCTCCCGTCCTGGACCCGAGTCGGGCCCATGGGAACCGGG
 - 5548 ALWN1, 5558 ESP1, 5564 SMAI XMAI, 5568 KPNI,
- LeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArg
 5582 CTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCGTGGCTCTCGG
 GAGATACCGTTACTCCCGACGCCCACCCGCCCTACCGAGAGAGGGGCACCGAGAGCC
- ProSerTrpGlyProThrAspProArgArgArgSerArgAsnLeuGlyLysVallleAsp
 5642 CCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTCATCGAT
 GGATCGACCCCGGGGTGTCTGGGGGCCCCATCCAGCGCGTTAAACCCATTCCAGTAGCTA
 - 5650 APAI, 5696 CLAI,
- ThrLeuThrCysGlyPheAlaAspLeuMetGlyTyrIleProLeuValOC AM
 5702 ACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCTAATAGTCGAC
 TGGGAATGCACGCCGAAGCGGCTGGAGTACCCCATGTATGGCGAGCAGATTATCAGCTG

5724 HGIE2, 5755 SALI,

FIG. 21-Page 10

3122	CGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCGGTTTGGGCGCGGCCGGACTATAACCCGGCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGCCAAACCCGCGCCGGCCTGATATTGGGC
	3143 ALWN1, 3164 EAG1 XMA3,
3182	ProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysProCCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTGCCCGGGCGATCACCTCTGCTGCACCAGGTACCGACGGGC
	3217 HGIE2, 3229 NCOI,
3242	LeuProProProLysSerProProValProProProArgLysLysArgThrValValLeuCTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTGGTCCTCGAAGGTGGAGGTGGAGGTGGAGGTGGAGGTGGAGGTGGAGGTGGAGGTGGAGGTGGAGGTGGAGGTGGAGGTGGAGGTGGAGGA
3302	ThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSer ACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAGCTCC TGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCGTCGAGG
	3332 SACI, 3346 HIND3,
3362	SerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGlyTCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCGCCC
3422	CysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluProTGCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCTGGAGGGGGAGCCTACGGGGGGGG
	3437 EAM11051,
3482	GlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGlu GGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAACGCGGAG CCCCTAGGCCTAGAATCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTGCGCCTC
	3484 BAMHI, 3485 BSAB1, 3487 BSPE1,
3542	AspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAla GATGTCGTGTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTGCGCC CTACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCACGCGG
	3589 DRA3, 3600 SAC2,
3602	AlaGluGluGlnLysLeuProlleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsn GCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCACCACAAT CGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTGGTGTTA
	3611 ALWN1, 3655 PFLM1,
	LeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAsp
3662	TTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACATTTGAC AACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGTAAACTG
3662	

FIG. 18-Page 6

2522	ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGlrCCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAGGGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTATTCCGTC
	2553 PSTI,
2582	ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGlnGTGGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAGCACCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGTC
	2594 DRA3,
2642	ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro GTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCC CAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGG
2702	ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrProCCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATACCCGGGGACGTTCGGGAACGACCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGC
	2757 HGIE2,
2762	ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeuGTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCATGCTCCATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTACGAG
	2809 AAT2,
2822	ThrAspProSerHislleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerProACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATCACCCTGACTAGGGAGGG
	2850 EAG1 XMA3,
2882	ProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG
	2889 BALI, 2903 NHEI,
2942	ThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln ACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAG TGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTC
	2966 ESP1, 2969 SACI,
3002	GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer GAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCC CTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTGAGG
3062	PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu TTCGATCCGCTTGTGGCGGAGGAGGACGAGGGGGGAGATCTCCGTACCCGCAGAAATCCTG AAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGAC
	3096 BGL2,
	ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro

2		AAACAAAAT	GGCTGCATAT	AlaAlaGlnGlyTyrLysValLeuValLeuAs GCAGCTCAGGGCTATAAGGTGCTAGTACTCAA CGTCGAGTCCCGATATTCCACGATCATGAGTT
	1 HIND3,	24 NDEI,	52 SCAI,	

- ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAsp 62 CCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATCGAT GGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTAGCTA
 - 116 CLAI,
- ProAsnileArgThrGlyValArgThrileThrThrGlySerProIleThrTyrSerThr
 122 CCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTCCACC
 GGATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAGGTGG
- TyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCys
 182 TACGGCAAGTTCCTTGCCGACGGCGGTGCTCGGGGGGGCGCTTATGACATAATATTTGT
 ATGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCCGCGAATACTGTATTATTAAACA
- AspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGln
 GACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCACTGTCCTTGACCAA
 CTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAACCGTGACAGGAACTGGTT
- ThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPhe
 362 ACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCTTTT
 TGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAGGGAAAA
- TyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHis
 TACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTGTCAT
 ATGCCGTTCCGATAGGGGGGGGCTTCATTAGTTCCCCCCCTCTGTAGAGTAGAAGACAGTA

FIG. 21-Page 1

- 4862 AGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGGCCTGCTACTCCATAGAA TCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTATCTT 4893 BGL2. ProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis 4922 CCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGAGGTG 4954 NCOI. SerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro 4982 AGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGTACCG TCAATGAGAGGTCCACTTTAGTTATCCCACCGGCGTACGGAGTCTTTTGAACCCCATGGC 5015 SPHI, 5035 KPNI, ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly 5042 CCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCCAGAGGA GGGAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGCGATCCGAAGACCGGTCTCCT 5064 APAI, 5091 BALI, GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys 5102 GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAAA CCGTCCCGACGGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCGAGTTT 5113 NDEI, LeuThrProIleAlaAlaAlaGlyGlnLeuAspLeuSerGlyTrpPheThrAlaGlyTyr 5174 NOTI, 5175 EAG1 XMA3, 5182 BALI, 5186 PVU2, SerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys AGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCCGCTGGATCTGGTTTTGC TCGCCCCTCTGTAAATAGTGTCGCACAGAGTACGGGCCGGGCCGACCTAGACCAAAACG 5240 DRA3, LeuLeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgMetSerThrAsn 5282 CTACTCCTGCTTGCTGCAGGGGTAGGCATCTACCTCCCCCAACCGAATGAGCACGAAT GATGAGGACGACGTCCCCATCCGTAGATGGAGGGGGTTGGCTTACTCGTGCTTA 5295 PSTI. ProLysProGlnArgLysThrLysArgAsnThrAsnArgArgProGlnAspValLysPhe 5342 CCTAAACCTCAAAGAAAGACCAAACGTAACACCAACCGGCGGCCGCAGGACGTCAAGTTC GGATTTGGAGTTTCTGGTTTGCATTGTGGTTGGCCGCCGCGTCCTGCAGTTCAAG 5380 NOTI, 5381 EAG1 XMA3, 5390 AAT2, 5401 SMAI XMAI,
- ProGlyGlyGlyGlnIleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeu
 5402 CCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCTAGATTG
 GGCCCACCGCCAGTCTAGCAACCACCTCAAATGAACAACGGCGCGTCCCCGGGATCTAAC

4229 DRD1, 4236 ALWN1,

GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer
4262 GAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAAGTCC
CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCGCACCGGTAGTTCAGG

4301 BGLI, 4308 BALI,

LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
4322 CTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGCGGC
GAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCTCTTGACGCCG

4345 APAI,

- TyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuVal
 4442 TACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCTCGTG
 ATGTAGTTCCGGGCCCGTCGGACAGCTCGGCGTCCCGAGGTCCTGACGTGGTACGAGCAC

4452 SMAI XMAI,

- CysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
 4502 TGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGGGGAGC
 ACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGCCGCTCG
 - 4508 DRD1, 4511 TTH3I,
- LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln
 4562 CTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCTGGGGACCCCCACAA
 GACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGGACCCCTGGGGGGTGTT
- ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp
 4622 CCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCACGAC
 GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTGCTG

4637 SACI,

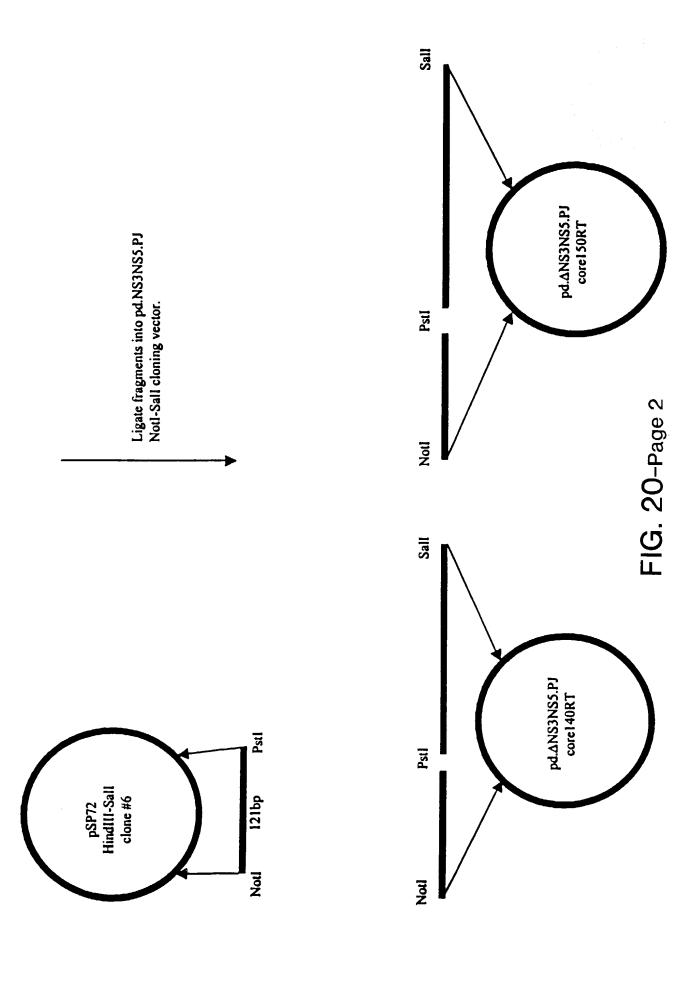
GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla
GGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGCGAGAGCT
CCGCGACCTTTCTCCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGGAGCGCTCTCGA

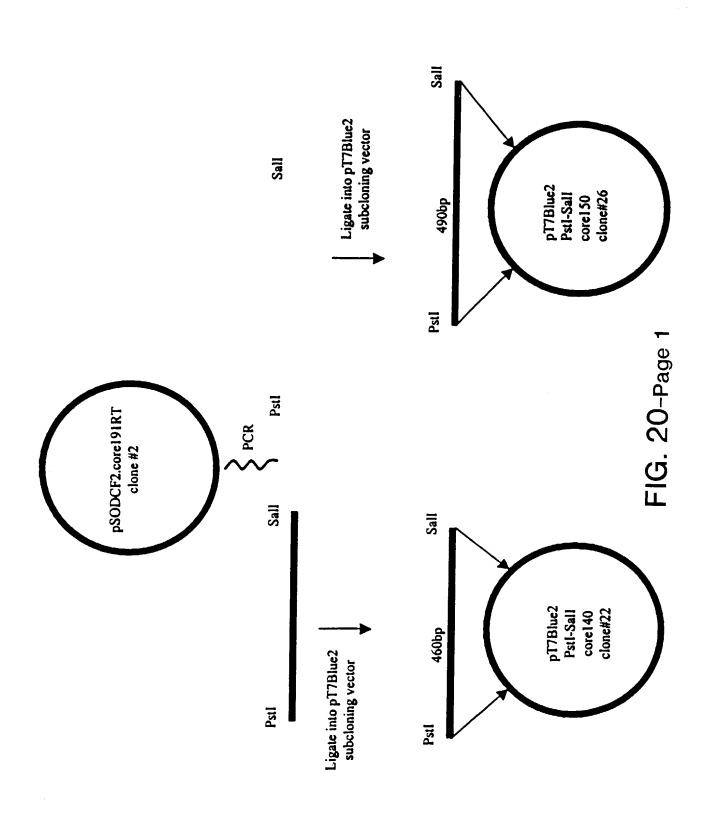
4731 NRUI,

- AlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe
 4742 GCGTGGGAGACAGCAAGACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT
 CGCACCCTCTGTCGTTCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTACAAA
- AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla 4802 GCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCC CGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAATATCGG

4806 PFLM1, 4807 DRA3,

ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu





ThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGly 1922 ACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTCGGC TGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGCCTCGGGAGCATCAGCCG 1928 TTH31. ${\tt ValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrp}$ 1982 GTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTGCAGTGG CACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCCGTCACGTCACC 2004 NAEI, 2017 SMAI XMAI, MetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrVal 2042 ATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCACTACGTG TACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGGGTGCGTGATGCAC 2067 SMAI XMAI, 2093 DRA3, ProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGln 2102 CCGGAGAGCGATGCAGCTGCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAACCCAG GGCCTCTCGCTACGTCGACGGCGCAGTGACGGTATGAGTCGTCGGAGTGACATTGGGTC 2115 PVU2, 2159 ALWN1, LeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer 2162 CTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGGTTCC GAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGGCCAAGG 2164 MST2, 2220 ECON1, ${\tt TrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu}$ 2222 TGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGGCTA ACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACTCGCTGAAATTCTGGACCGAT $Lys \verb|AlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArgGlyTyr|$ AAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCTTTGTGTCCTGCCAGCGCGGGTAT 2282 TTTCGATTCGAGTACGGTGTCGACGGACCCTAGGGGAAACACAGGACGGTCGCGCCCATA 2285 ESP1, 2300 PVU2, 2310 BAMHI, ${\tt LysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle}$ AAGGGGGTCTGGCGAGGGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGAGATC TTCCCCCAGACCGCTCCCCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAG ${\tt ThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArgThrCysArgAsnMet}$ 2402 ACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGGAACATG TGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGCCAGGATCCTGGACGTCCTTGTAC 2425 BSAB1, 2441 AVR2, 2448 SSE83871, 2449 PSTI, TrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAla 2462 TGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTTCCTGCG ACCTCACCCTGGAAGGGGTAATTACGGATGTGGTGCCCGGGGACATGGGGGGAAGGACGC

2480 ASE1, 2497 APAI,

	CAGTGCTCGTGGACCC	ACGAGCAACCGCCGC	AGGACCGACGAAA	CCGCCCCATAACGGAC
--	------------------	-----------------	---------------	------------------

SerThrGlyCysValVallleValGlyArgValValLeuSerGlyLysProAlallelle
1322 TCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAATCATA
AGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGTTAGTAT

1369 NAEI,

- ProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeu
 1382 CCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTA
 GGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACCTTCTCACGAGAGTCGTGAAT

 1385 DRD1.
- ProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeu
 1442 CCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTC
 GGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAGCCGGAG
- LeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGln
 1502 CTGCAGACCGCGTCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAACTGGCAA
 GACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTGACCGTT

 ^
 1502 PSTI, 1507 TTH31,
- LysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyrLeu
 1562 AAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATACTTG
 TTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTTATGAAC
 ^

1565 XHOI, 1586 NDEI,

AlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAla GCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGCT CGCCCGAACAGTTGCGACGACCATTGGGGCGGTAACGAAGTAACTACCGAAAATGTCGA

1643 BSTE2, 1677 ALWN1 PVU2,

- AlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrp
 1682 GCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGGGGGTGG
 CGACAGTGGTCGGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCCCCCACC
- ValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeuAla
 1742 GTGGCTGCCCAGCTCGCCCCCGGTGCCGACCGCTTTGTGGGCGCTTAGCT
 CACCGACGGGTCGAGCGGGGGCCACGGCGATGACGGAAACACCCGCGACCGAATCGA

1794 ESP1,

GlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGlyTyr
1802 GGCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGACATCCTTGCAGGGTAT
CCGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGTCCCATA

1802 KASI NARI,

GlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValProSer 1862 GGCGCGGGCGGGGGGGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCCCTCC CCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGGAGG

1878 SACI, 1899 BSPH1,

FIG. 18-Page 3

 ${ t LysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle}$ 2342 AAGGGGGTCTGGCGAGGGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGAGATC TTCCCCCAGACCGCTCCCCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAG $Thr {\tt Gly His Val Lys As n Gly Thr Met Arg Ile Val Gly Pro Arg Thr Cys Arg As n Met}$ 2402 ACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGGAACATG TGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGCCAGGATCCTGGACGTCCTTGTAC 2425 BSAB1, 2441 AVR2, 2448 SSE83871, 2449 PSTI, TrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAla 2462 TGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTTCCTGCG ACCTCACCCTGGAAGGGGTAATTACGGATGTGGTGCCCGGGGACATGGGGGGAAGGACGC 2480 ASE1, 2497 APAI, ${\tt ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln}$ 2522 CCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAG GGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTATTCCGTC 2553 PSTI, ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln 2582 GTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG CACCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGTC 2594 DRA3, ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro 2642 GTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCC CAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGG ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro 2702 CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATACCCG GGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGC 2757 HGIE2, ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCATGCTC CATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTACGAG 2809 AAT2. ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerPro 2822 ACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATCACCC TGACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCCGCTTCCAACCGCTCCCCTAGTGGG 2850 EAG1 XMA3, ProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys 2882 CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG

2889 BALI, 2903 NHEI,

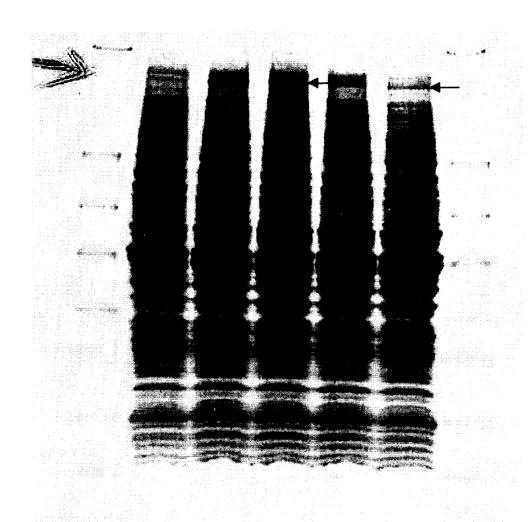


FIG. 19

1742	ValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeuAl GTGGCTGCCCAGCTCGCCCCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGCTTAGC CACCGACGGGTCGAGCGGGGGGCCACGGCGATGACGAAACACCCGCGACCGAATCG
	1794 ESP1,
1802	GlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGlyTyrGGCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGACATCCTTGCAGGGTATCCGCGGGGGGGG
	1802 KAS1 NARI,
1862	GlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValProSerGCGCGGGGCGTGGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCCCTCCCCGCGCCCCCCCC
	1878 SACI, 1899 BSPH1,
1922	ThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGlyAcGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTCGGCTGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCATCAGCCG
	1928 TTH3I,
1982	ValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrp GTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTGCAGTGG CACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCCCGTCACGTCACC
	2004 NAEI, 2017 SMAI XMAI,
,,2042	MetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrVal ATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCACTACGTG TACTTGGCCGACTATCGGAAGCGGAGGCCCCCTTGGTACAAAGGGGGTGCGTGATGCAC
	2067 SMAI XMAI, 2093 DRA3,
2102	ProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGln CCGGAGAGCGATGCAGCTGCCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAACCCAG GGCCTCTCGCTACGTCGACGGGCGCAGTGACGGTATGAGTCGTCGGAGTGACATTGGGTC
	2115 PVU2, 2159 ALWN1,
2162	LeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer CTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGGTTCC GAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGGCCAAGG
	2164 MST2, 2220 ECON1,
2222	TrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu TGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGGCTA ACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACTCGCTGAAATTCTGGACCGAT
2282	LysAlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArgGlyTyr AAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCTTTGTGTCCTGCCAGCGCGGGTAT TTTCGATTCGA
	2285 ESP1, 2300 PVU2, 2310 BAMHI,

FIG. 17-Page 4

TCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACCTTCAC	
-1 CCCGAG1 1 CGGGGAGGGGG1AGCACCC 1 GG1C 1 ACACC 1 1 CACA	AAACTAAGU.GGAGTTC

- ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle
 1142 CCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAAATC
 GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAG

 1150 NCOI,
- ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu
 1262 GTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTATTGCCTG
 CAGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGACGAAACCGGCGCATAACGGAC
- SerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIleIle
 1322 TCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAATCATA
 AGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGTTAGTAT

 1369 NAEI.
- ProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeu
 1382 CCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTA
 GGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTCTCACGAGAGTCGTGAAT

 1385 DRD1,
- ProTyrlleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeu
 1442 CCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTC
 GGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAGCCGGAG
- LeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGln
 1502 CTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAACTGGCAA
 GACGTCTGGCGCAGGCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTGACCGTT

 ^
 1502 PSTI, 1507 TTH31,
- LysLeuGluThrPheTrpAlaLysHisMetTrpAsnPhelleSerGlylleGlnTyrLeu
 1562 AAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATACTTG
 TTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTTATGAAC

 1565 XHOI, 1586 NDEI.
- AlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAla GCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGCT CGCCCGAACAGTTGCGACGACCATTGGGGCGGTAACGAAGTAACTACCGAAAATGTCGA
 - 1643 BSTE2, 1677 ALWN1 PVU2,
- AlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrp
 1682 GCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGGGGGTGG
 CGACAGTGGTCGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCCCCCACC

- ThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIle 662 ACGTGTGTCACCCAGACAGTCGATTCAGCCTTGACCCTACCTTCACCATTGAGACAATC TGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTCTGTTAG ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys ACGCTCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGGGAGGACTGGCAGGGGGAAG TGCGAGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCCCCCTTC ProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSer CCAGGCATCTACAGATTTGTGGCACCGGGGGGGGGCCCCCTCCGGCATGTTCGACTCGTCC GGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTGAGCAGG 816 BGLI, 833 DRD1, ValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThr 881 SACI. ThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu 902 ACAGTTAGGCTACGAGCGTACATGAACACCCGGGGCTTCCCGTGTGCCAGGACCATCTT TGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTGGTAGAA 931 SMAI XMAI, GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln 962 GAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCCAG CTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTC 985 STUI. 1022 ACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCT TGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCACACGCGA 1069 DRA3, ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys AGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCTCAAG 1082 TCCCGAGTTCGGGGAGGGGGTAGCACCTTGGTCTACACCTTCACAAACTAAGCGGAGTTC ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle CCCACCCTCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAAATC GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAG 1150 NCOI, ThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeuGluVal ^ ^ 1230 BSPH1, 1234 DRD1, 1237 AVA3, 1245 EAG1 XMA3, 1250 DRD1,
- ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu 1262 GTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTATTGCCTG

ProSerTrpGlyProThrAspProArgArgArgAsnLeuGlyLysValIleAsp
5642 CCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTCATCGAT
GGATCGACCCCGGGGTGTCTGGGGGCCCGCATCCAGCGCGTTAAACCCATTCCAGTAGCTA

5650 APAI, 5696 CLAI,

ThrLeuThrCysGlyPheAlaAspLeuMetGlyTyrIleProLeuValGlyAlaProLeu
5702 ACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCCTCTT
TGGGAATGCACGCCGAAGCGGCTGGAGTACCCCATGTATGGCGAGCAGCCGCGGGGAGAA

5724 HGIE2, 5750 KAS1 NARI, 5756 ECON1,

GlyGlyAlaAlaArgAlaLeuAlaHisGlyValArgValLeuGluAspGlyValAsnTyr 5762 GGAGGCGCTGCCAGGGCCCTGGCGCATGCCGCGGTTCTGGAAGACGGCGTGAACTAT CCTCCGCGACGGTCCCGGGACCGCTACCGCAGGCCCAAGACCTTCTGCCGCACTTGATA

5772 BSTXI, 5775 APAI,

AlaThrGlyAsnLeuProGlyCysSerOC AM
5822 GCAACAGGGAACCTTCCTGGTTGCTCTTAATAGTCGAC
CGTTGTCCCTTGGAAGGACCAACGAGAATTATCAGCTG

5854 SALI,

FIG. 18-Page 10

5042	ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGl CCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCCAGAGG GGGAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGCGATCCGAAGACCGGTCTCCT
	5064 APAI, 5091 BALI,
5102	GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLysGGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAAACCGTCCCGACGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCGAGTTT
	5113 NDEI,
5162	LeuThrProlleAlaAlaAlaGlyGlnLeuAspLeuSerGlyTrpPheThrAlaGlyTyrCTCACTCCAATAGCGGCCGCTGGCCAGCTGGACTTGTCCGGCTGGTTCACGGCTGGCT
	5174 NOTI, 5175 EAG1 XMA3, 5182 BALI, 5186 PVU2,
5222	SerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys AGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCCGCTGGATCTGGTTTTGC TCGCCCCCTCTGTAAATAGTGTCGCACAGAGTACGGGCCGGGGCGACCTAGACCAAAACG
	5240 DRA3,
5282	LeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgMetSerThrAsn CTACTCCTGCTTGCTGCAGGGGTAGGCATCTACCTCCTCCCCAACCGAATGAGCACGAAT GATGAGGACGAACGACGTCCCCATCCGTAGATGGAGGAGGGGTTGGCTTACTCGTGCTTA
	5295 PSTI,
5342	ProLysProGlnArgLysThrLysArgAsnThrAsnArgArgProGlnAspValLysPhe CCTAAACCTCAAAGAAAGACCAAACGTAACACCAACCGGCGGCCGCAGGACGTCAAGTTC GGATTTGGAGTTTCTTGTTTGCATTGTGGTTGGCCGCCGGCGTCCTGCAGTTCAAG
	5380 NOTI, 5381 EAG1 XMA3, 5390 AAT2, 5401 SMAI XMAI,
5402	ProGlyGlyGlyGlnIleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeuCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCTAGATTGGCCCCCACCCCAGGTCTAGCAACCACCTCAAATGAACAACGGCGCGTCCCCGGGATCTAAC
	5449 APAI,
5462	GlyValArgAlaThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnPro GGTGTGCGCGCGACGAGAAAGACTTCCGAGCGTCGCAACCTCGAGGTAGACGTCAGCCT CCACACGCGCGCTGCTCTTTCTGAAGGCTCGCCAGCGTTGGAGCTCCATCTGCAGTCGGA
	5467 BSSH2, 5478 XMNI, 5502 XHOI, 5511 AAT2,
5522	IleProLysAlaArgArgProGluGlyArgThrTrpAlaGlnProGlyTyrProTrpProATCCCCAAGGCTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGGCCCTAGGGGTTCCGAGCAGCCGGGCTCCCGTCCTGGACCCGAGTCGGGCCCATGGGAACCGGG
	5548 ALWN1, 5558 ESP1, 5564 SMAI XMAI, 5568 KPNI,
5582	LeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArg CTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCTCCCCGTGGCTCTCGG GAGATACCGTTACTCCCGACGCCCCACCCGCCCTACCGAGGACAGAGGGGCACCGAGAGCC

2	MetAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAsn AGCTTACAAAACAAAATGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTCAAC TCGAATGTTTTGTTT
	1 HIND3, 24 NDEI, 52 SCAI,
62	ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAsp CCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATCGAT GGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTAGCTA
	116 CLAI,
122	ProAsnileArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThr CCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTCCACC GGATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAGGTGG
182	TyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCys TACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGGCGCTTATGACATAATATTTGT ATGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCCGCGAATACTGTATTATAAACA
242	AspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGln GACGAGTGCCACTCCACGGATGCCACATCCATCTTGGCCATTTGGCCACTGTCCTTGACCAA CTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAACCGTGACAGGAACTGGTT
302	AlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySerVal GCAGAGACTGCGGGGGGGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTCCGTC CGTCTCTGACGCCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCCGAGGCAG
	303 ALWN1,
362	ThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPhe ACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCTTTT TGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAGGGAAAA
422	TyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHis TACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTGTCAT ATGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCCTCTGTAGAGTAGAAGACAGTA
482	SerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaVal TCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGCCGTG AGTTTCTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACGGCAC

AlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerVallleAspCysAsn
GCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGATGACTGCAAT
CGTTGGCTACGGGGATACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTA

 ${\tt AlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValValVal}$

GCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGTCGTG CGGATGATGGCGCCAGAACTGCACAGCAGTAGGGCTGGTCGCCGCTACAACAGCAGCAC

615 BSPH1,

550 SAC2, 560 DRD1,

542

- SerLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaVal
 TCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGCCGTG
 AGTTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACGGCAC
- AlaTyrTyrArgGlyLeuAspValSerVallleProThrSerGlyAspValValValVal
 542 GCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGTCGTG
 CGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGCTACAACAGCAGCAC

550 SAC2, 560 DRD1,

AlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerVallleAspCysAsn 602 GCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTGCAAT CGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTA

615 BSPH1,

- ThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIle
 662 ACGTGTGTCACCAGACAGTCGATTTCAGCCTTGACCCTTCACCATTGAGACAATC
 TGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTCTGTTAG
- ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys
 ACGCTCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGCCAGGGGGAAG
 TGCGAGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCCCCCTTC
- ProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSer
 CCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCGGCATGTTCGACTCGTCC
 GGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTGAGCAGG

816 BGLI, 833 DRD1,

881 SACI,

ThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu
902 ACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCATCTT
TGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTGGTAGAA

931 SMAI XMAI.

GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln 962 GAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCCAG CTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTC

985 STUI,

ThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAla 1022 ACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCT TGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCACACGCGA

1069 DRA3,

ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys
1082 AGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCTCAAG

2522	CCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAGGGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTATTCCGTC
	2553 PSTI,
2582	ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGlnGTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAGCCA
	2594 DRA3,
2642	ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaProGTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCCCCAGGGTAGCGGGCTTAAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGG
2702	ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrProCCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATACCCGGGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGC
	2757 HGIE2,
2762	ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeuGTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCATGCTCCATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTACGAG
	2809 AAT2,
2822	ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerProAcTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATCACCCTGACTAGGGAGGG
	2850 EAG1 XMA3,
2882	ProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG
	2889 BALI, 2903 NHEI,
2942	ThralaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGlnACCGCTAACCATGACTCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAGTGGGGGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTC
	2966 ESP1, 2969 SACI,
3002	GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer GAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCC CTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTGAGG
3062	PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu TTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAAATCCTG AAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGAC
	3096 BGL2,
3122	ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnProCGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAACCCC

FIG. 14-Page 5

	MetAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAsr
2	AGCTTACAAAACAAAATGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTCAAC
	TCGAATGTTTTGTTTTACCGACGTATACGTCGAGTCCCGATATTCCACGATCATGAGTTC
	^

1 HIND3, 24 NDEI, 52 SCAI,

ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAsp 62 CCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATCGAT GGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTAGCTA

116 CLAI,

- ProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThr
 122 CCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTCCACC
 GGATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAGGTGG
- TyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCys
 TACGGCAAGTTCCTTGCCGACGGCGGTGCTCGGGGGGGCGCTTATGACATAATAATTTGT
 ATGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCCGCGAATACTGTATTATTAAACA
- AspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGln
 GACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCACTGTCCTTGACCAA
 CTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAACCGTGACAGGAACTGGTT
- AlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySerVal
 GCAGAGACTGCGGGGGGGGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTCCGTC
 CGTCTCTGACGCCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCCGAGGCAG

 303 ALWN1.
- ThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPhe
 ACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCTTTT
 TGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAGGGAAAA

FIG. 17-Page 1

TyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuVal TACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCTCGTG ATGTAGTTCCGGGCCCGTCGGACAGCTCGGCGTCCCGAGGTCCTGACGTGGTACGAGCAC 4452 SMAI XMAI, CysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSer 4502 TGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGCGAGC ACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGCCGCTCG 4508 DRD1, 4511 TTH31, LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln 4562 CTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCTGGGGACCCCCCACAA ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp CCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCACGAC 4622 GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTGCTG 4637 SACI, GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla 4682 GGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGCGAGAGCT CCGCGACCTTTCTCCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGGGAGCGCTCTCGA 4731 NRUI, AlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe 4742 GCGTGGGAGACAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT CGCACCCTCTGTCGTTCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTACAAA AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla 4802 GCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCC CGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAATATCGG 4806 PFLM1, 4807 DRA3, ${\tt ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu}$ 4862 AGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCATAGAA TCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTATCTT 4893 BGL2. ProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis 4922 CCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGAGGTG 4954 NCOI. SerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro 4982 AGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGTACCG TCAATGAGAGGTCCACTTTAGTTATCCCACCGGCGTACGGAGTCTTTTGAACCCCATGGC

5015 SPHI, 5035 KPNI,

5449 APAI,

GlyValArgAlaThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnPro
5462 GGTGTGCGCGACGAGAAAGACTTCCGAGCGTCGCAACCTCGAGGTAGACGTCAGCCT
CCACACGCGCGCTGCTCTTCTGAAGGCTCGCAGCGTTGGAGCTCCATCTGCAGTCGGA

5467 BSSH2, 5478 XMNI, 5502 XHOI, 5511 AAT2,

IleProLysAlaArgArgProGluGlyArgThrTrpAlaGlnProGlyTyrProTrpPro
ATCCCAAGGCTCGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGGCCC
TAGGGGTTCCGAGCAGCCGGGCTCCCGTCCTGGACCCGAGTCGGGCCCATGGGAACCGGG

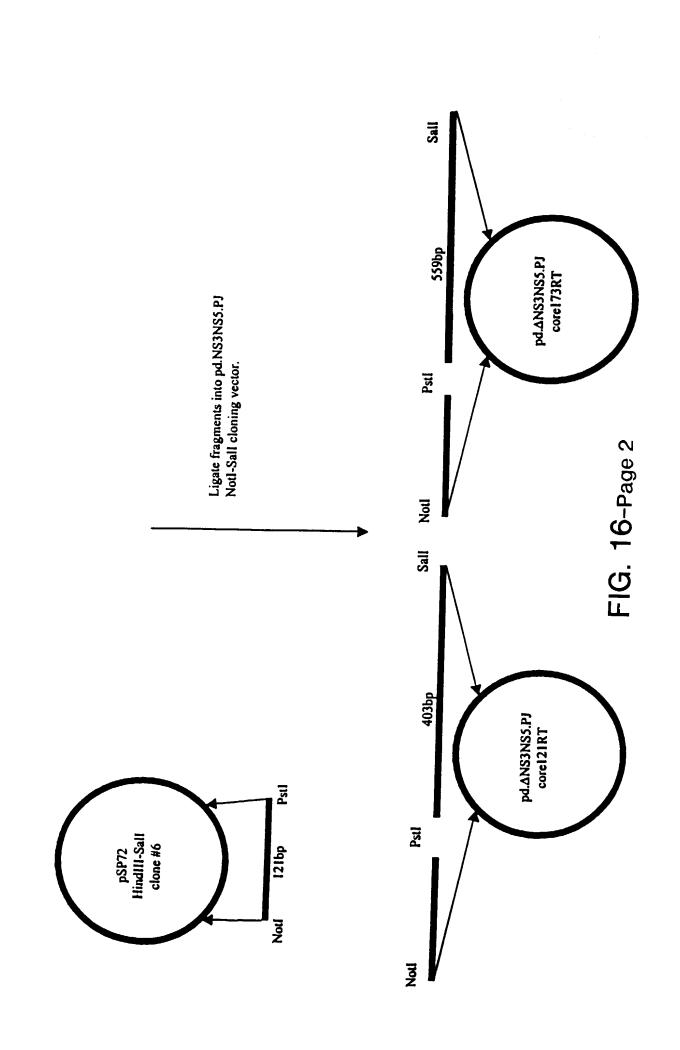
5548 ALWN1, 5558 ESP1, 5564 SMAI XMAI, 5568 KPNI,

- LeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArg
 5582 CTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCGTGGCTCTCGG
 GAGATACCGTTACTCCCGACGCCCACCCGCCCTACCGAGACAGAGGGGCACCGAGAGCC

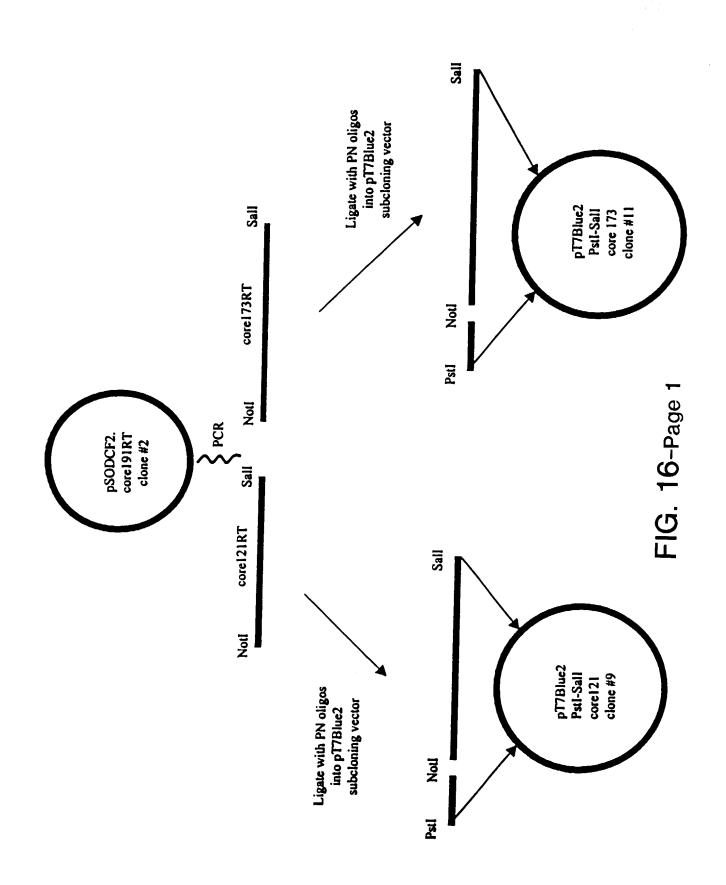
5650 APAI, 5698 SALI,

5702 AC TG

FIG. 17-Page 10



1322	4862	AGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGGCCTGCTACTCCATAGAA TCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTATCTT
		4893 BGL2,
1382	4922	ProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis CCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGAGGTG
		4954 NCOI,
1442	4982	SerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro AGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGTACCG TCAATGAGAGGTCCACTTTAGTTATCCCACCGGCGTACGGAGTCTTTTGAACCCCATGGC
		5015 SPHI, 5035 KPNI,
1502	5042	ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly CCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCCAGAGA GGGAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCCGCGATCCGAAGACCGGTCTCCT
		5064 APAI, 5091 BALI,
1562	5102	GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAAA CCGTCCCGACGGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCGAGTTT
		5113 NDEI,
1622	5162	LeuThrProlleAlaAlaAlaGlyGlnLeuAspLeuSerGlyTrpPheThrAlaGlyTyrCTCACTCCAATAGCGGCCGGCCGGCCAGCTGGACTTGTCCGGCTGGTTCACGGCTGCTACGAGTGAGGGCCGACCAAGTGCCGACCGA
		5174 NOTI, 5175 EAG1 XMA3, 5182 BALI, 5186 PVU2,
1682	5222	SerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys AGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCCGCTGGATCTGGTTTTGC TCGCCCCCTCTGTAAATAGTGTCGCACAGAGTACGGGCCGGGCGACCTAGACCAAAACG
1742		5240 DRA3,
	5282	LeuLeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgMetSerThrAsn CTACTCCTGCTTGCTGCAGGGGTAGGCATCTACCTCCTCCCCAACCGAATGAGCACGAAT GATGAGGACGAACGACGTCCCCATCCGTAGATGGAGGAGGGGTTGGCTTACTCGTGCTTA
1802		5295 PSTI,
	5342	ProLysProGlnArgLysThrLysArgAsnThrAsnArgArgProGlnAspValLysPhe CCTAAACCTCAAAGAAAGACCAAACGTAACACCAACCGGCGGCGCCGCAGGACGTCAAGTTC GGATTTGGAGTTTCTTGTTTTCTGGTTTGCATTGTGGTTGGCCGCCGGCGTCCTGCAGTTCAAG
1862		5380 NOTI, 5381 EAG1 XMA3, 5390 AAT2, 5401 SMAI XMAI,
	3402	ProGlyGlyGlyGlnIleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeu CCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCTAGATTG GGCCCACCGCCAGTCTAGCAACCACCTCAAATGAACAACGGCGCGTCCCCGGGATCTAAC



4229 DRD1, 4236 ALWN1,

GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer 4262 GAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAAGTCC CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCGCACCGGTAGTTCAGG

4301 BGLI, 4308 BALI,

LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
4322 CTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGCGGC
GAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCTCTTGACGCCG

4345 APAI,

- TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys
 4382 TATCGCAGGTGCCGCGCGGGGGGGGTACTGACAACTAGCTGTGGTAACACCCTCACTTGC
 ATAGCGTCCACGGCGCGCTCGCCGCATGACTGTTGATCGACACCATTGTGGGAGTGAACG
- TyrileLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuVal
 TACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCTCGTG
 ATGTAGTTCCGGGCCCGTCGGACAGCTCCGGCGTCCCGAGGTCCTGACGTGGTACGAGCAC

4452 SMAI XMAI,

- CysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
 4502 TGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGGGGGGAGC
 ACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGCCGCTCG
 - 4508 DRD1, 4511 TTH3I,
- LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln
 4562 CTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCCTGGGGACCCCCACAA
 GACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGGGACCCCTGGGGGGTGTT
- ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp
 4622 CCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCACGAC
 GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTGCTG

4637 SACI,

GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla 4682 GGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCCTACAACCCCCCTCGCGAGAGCT CCGCGACCTTTCTCCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGGAGCGCTCTCGA

4731 NRUI,

- AlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe GCGTGGGAGACAGCAAGACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT CGCACCCTCTGTCGTTCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTACAAA
- AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla GCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCC CGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAATATCGG

4806 PFLM1, 4807 DRA3,

ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu

3589 DRA3, 3600 SAC2,

- AlaGluGluGlnLysLeuProlleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsn GCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCACCACAAT CGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTGGTGTTA
 - 3611 ALWN1, 3655 PFLM1,
- LeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAsp
 TTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACATTTGAC
 AACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGTAAACTG

 3681 DRA3.
- ArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAla 3722 AGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAGCGGCG TCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTTCGTCGCCGC
- SerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProProHis
 TCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCACAC
 AGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGGTGTG
 - 3816 HIND3,
- SerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAla
 TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAAGGCC
 AGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTCCGG
 - 3875 AAT2, 3890 BGLI,
- ValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIleAsp
 3902 GTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAATAGAC
 CATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTATCTG
- ThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys
 3962 ACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGGTCGTAAG
 TGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCAGCATTC
- ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu 4022 CCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATGGCTTTG GGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTACCGAAAC
- TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr 4082 TACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCAATAC ATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAGGTTATG
- SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet TCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCCAATG AGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGGGGTTAC
 - 4160 ECORI,
- GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr 4202 GGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACG CCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAGGCATGC

2942	ThralaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln CCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAG TGGCGATTGGTACTGAGGGGACTACGACTCCGAGTATCTCCGGTTGGAGGATACCTCCGTC
	2966 ESP1, 2969 SACI,
3002	GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer GAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCC CTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTGAGG
3062	PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu TTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAAATCCTG AAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGAC
	3096 BGL2,
3122	ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnProCGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAACCCCGCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGCCAAACCCGCGCCGGCCTGATATTGGGG
	3143 ALWN1, 3164 EAG1 XMA3,
3182	ProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysPro CCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTGCCCG GGCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCGACGGGC
	3217 HGIE2, 3229 NCOI,
3242	LeuProProProLysSerProProValProProProArgLysLysArgThrValValLeu CTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTGGTCCTC GAAGGTGGAGGTTTCAGGGGAGGACACGGAGGCGGAGCCTTCTTCGCCTGCCACCAGGAG
3302	ThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSer ACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAGCTCC TGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCGTCGAGG
	3332 SACI, 3346 HIND3,
3362	SerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGly TCAACTTCCGGCATTACGGGCGACAATACGACATCCTCTGAGCCCGCCC
3422	CysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluPro TGCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCTGGAGGGGGAGCCT ACGGGGGGGGGG
	3437 EAM11051,
3482	GlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGlu GGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAACGCGGAG CCCCTAGGCCTAGAATCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTGCGCCTC
	3484 BAMHI, 3485 BSAB1, 3487 BSPE1,
3542	AspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAla GATGTCGTGTGCTCCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTGCGCC CTACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCACGCGG

FIG. 17-Page 6

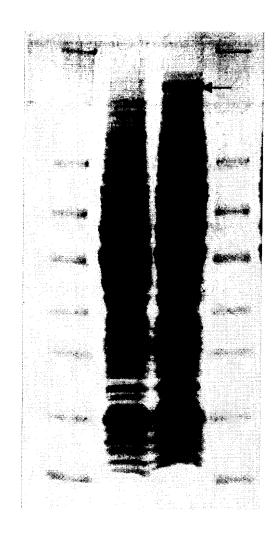


FIG. 15

- 662 ACGTGTGTCACCCAGACAGTCGATTCAGCCTTGACCCTTCACCATTGAGACAATC TGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTCTGTTAG ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys 722 ACGCTCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGGCAGGACTGGCAGGGGGAAG TGCGAGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCCCCCTTC ${\tt ProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSer}$ CCAGGCATCTACAGATTTGTGGCACCGGGGGGGGGCGCCCCTCCGGCATGTTCGACTCGTCC 816 BGLI, 833 DRD1, ${\tt ValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThr}$ 842 881 SACI, ThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu ACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCATCTT TGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTGGTAGAA 931 SMAI XMAI, GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln 962 GAATTTTGGGAGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCCAG CTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTC 985 STUI, ThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAla 1022 ACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCT TGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCACACGCGA 1069 DRA3, ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys 1082 AGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCTCAAG TCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACCTTCACAAACTAAGCGGAGTTC ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle 1142 CCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAAATC GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAG 1150 NCOI, ThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeuGluVal 1202 1230 BSPH1, 1234 DRD1, 1237 AVA3, 1245 EAG1 XMA3, 1250 DRD1,
 - FIG. 14-Page 2

ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeuGTCACGAGCACCTGGGTGCTCGTTGGCCGCGTCCTGGCCGCCTATTGCCTG

CAGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGACGAAACCGGCGCATAACGGAC

1262

- CCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCCAGAGGA GGGAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGCGATCCGAAGACCGGTCTCCT 5064 APAI, 5091 BALI,
- GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys
 5102 GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAAA
 CCGTCCCGACGGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCGAGTTT
 5113 NDEI.
- SerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys
 5222 AGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCCGCTGGATCTGGTTTTGC
 TCGCCCCCTCTGTAAATAGTGTCGCACAGAGTACGGGCCGGGGCGACCTAGACCAAAACG
- LeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgOP
 5282 CTACTCCTGCTGCAGGGGTAGGCATCTACCTCCTCCCCAACCGATGAATAGTCGAC
 GATGAGGACGAACGACGTCCCATCCGTAGATGGAGGGGGTTGGCTACTTATCAGCTG

5295 PSTI, 5336 SALI,

5240 DRA3,

FIG. 14-Page 9

4442	TyrlleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuVa TACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCTCGTC ATGTAGTTCCGGGCCCGTCGGACAGCTCGGCGTCCCGAGGTCCTGACGTGCTACGAGCAC
	4452 SMAI XMAI,
4502	CysGlyAspAspLeuValVallleCysGluSerAlaGlyValGlnGluAspAlaAlaSer TGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGCGAGG ACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGCCGCTCG
	4508 DRD1, 4511 TTH3I,
4562	LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGlnCTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCTGGGGACCCCCACAAGACTCCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGGGACCCCTGGGGGGTGTT
4622	ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp CCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCACGAC GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTGCTG
	4637 SACI,
4682	GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla GGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGCGAGAGCT CCGCGACCTTTCTCCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGGGAGCGCTCTCGA
	4731 NRUI,
4742	AlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe GCGTGGGAGACAGCACACCCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT CGCACCCTCTGTCGTTCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTACAAA
4802	AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla GCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCC CGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAATATCGG
	4806 PFLM1, 4807 DRA3,
4862	ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGluAGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCATAGAATCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTATCTT
	4893 BGL2,
4922	ProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis CCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGAGGTG
	4954 NCOI,
4982	SerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro AGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGTACCG TCAATGAGAGGTCCACTTTAGTTATCCCACCGGCGTACGGAGTCTTTTGAACCCCATGGC
	5015 SPHI. 5035 KPNI.

FIG. 14-Page 8

 ${\tt ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly}$

1884 SACI, 1905 BSPH1,

- ProSerThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuVal
 1922 CCCTCCACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTA
 GGGAGGTGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCAT
 1934 TTH31,
- ValGlyValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaVal 1982 GTCGGCGTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTG CAGCCGCACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCCCGTCAC

2010 NAEI, 2023 SMAI XMAI,

GlnTrpMetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHis
CAGTGGATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCAC
GTCACCTACTTGGCCGACTATCGGAAGCGGAGGCCCCCTTGGTACAAAGGGGGTGCGTG

2073 SMAI XMAI, 2099 DRA3,

TyrValProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrVal
TACGTGCCGGAGAGCGATGCAGCTGCCCGCGTCACTGCATACTCAGCAGCCTCACTGTA
ATGCACGGCCTCTCGCTACGTCGACGGCGCAGTGACGTTATGAGTCGTCGGAGTGACAT

2121 PVU2,

- ThrGlnLeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSer
 ACCCAGCTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCC
 TGGGTCGAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGG

 2165 ALWN1, 2170 MST2,
- GlySerTrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThr
 2222 GGTTCCTGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACC
 CCAAGGACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACTCGCTGAAATTCTGG

 2226 ECON1,
- GlyTyrLysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAla 2342 GGGTATAAGGGGGTCTGGCGAGGGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCT CCCATATTCCCCCAGACCGCTCCCCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGA
- GluileThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArgThrCysArg
 GAGATCACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGG
 CTCTAGTGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGCCAGGATCCTGGACGTCC

2431 BSAB1, 2447 AVR2, 2454 SSE83871, 2455 PSTI,

2	MetAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAs AGCTTACAAAACAAAATGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTCAA TCGAATGTTTTGTTT
	1 HIND3, 24 NDEI, 52 SCAI,
62	ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAsp CCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATCGA GGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTAGCTA
	116 CLAI,
122	ProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThrCCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTCCACGGGATTGTTAATGGTGACCGTCGGGGTAGTGCATGAGGTGCGGGGTAGTGCATGAGAGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGAGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGTGCATGAGGGTAGTGCATGAGGGTAGTGCATGAGGGTGCATGAGGAGGTGCATGAGGGTAGTGCATGAGGGTGCATGAGGGTAGTGCATGAGGGTGCATGAGGGTAGTGAGGGTAGTGCATGAGGGTAGTGCATGAGGGTGCATGAGGGTAGTGCATGAGGGTGCATGAGGGTAGTGAGGGTGCATGAGGGTAGTGAGGGTGAGTGCATGAGGGTAGTGAGGGTAGTGAGGGTAGTGAGGGTAGTGAGGGTAGTGAGGGTAGGGGTAGTGAGGGTAGGAGG
182	TyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCysTACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGGCGCTTATGACATAATTTGTATGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCCGCGAATACTGTATTATAAACA
242	AspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGlm GACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCACTGTCCTTGACCAA CTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAACCGTGACAGGAACTGGTT
302	AlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySerValGCAGAGACTGCGGGGGGGGGGGGGGGCTCCGTCCGCCACCCCCCCC
	303 ALWN1,
362	ThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPhe ACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCTTTT TGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAGGGAAAA
422	TyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHis TACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTGTCAT ATGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCCC
482	SerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaVal TCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGCCGTG AGTTTCTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACGGCAC
542	AlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValValValGCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGTCGTGCGGATGATGGCGCCAGAACAGCAGCAGCACACAGCAGCACACACA
	550 SAC2, 560 DRD1,
602	AlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerVallleAspCysAsn GCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTGCAAT CGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTA
	615 BSPH1,

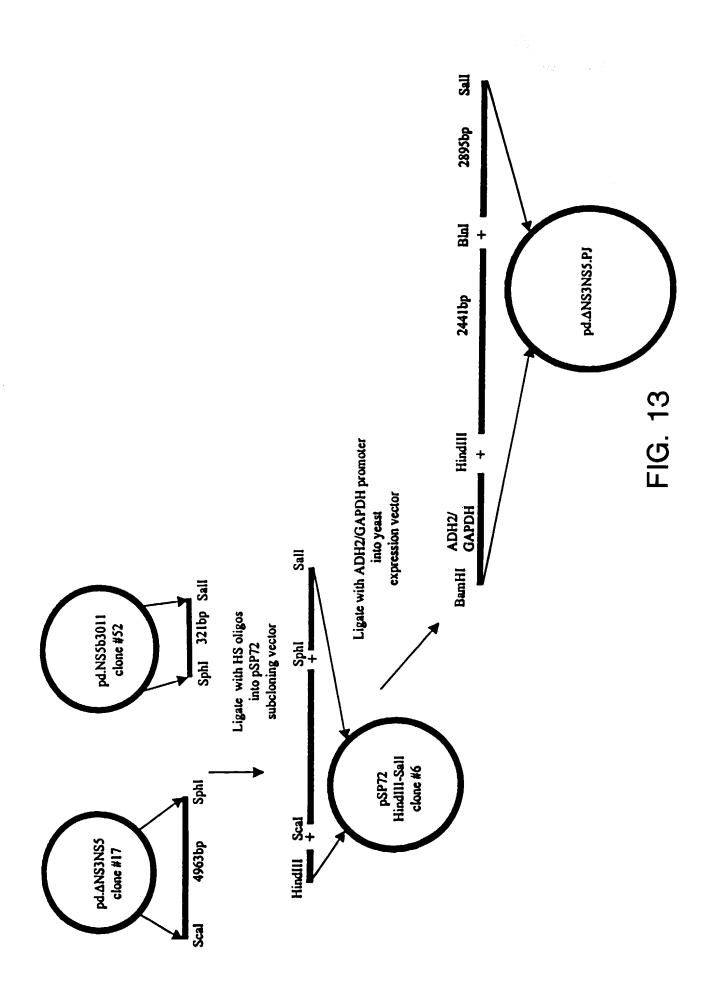
FIG. 14-Page 1

 $Thr {\tt CysValThr GlnThr Val AspPhe Ser Leu AspProThr Phe Thr I leGluThr I l$

1322	CysLeuSerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAla TGCCTGTCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCA ACGGACAGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGT
	1375 NAEI,
1382	IleIleProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGln ATCATACCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAG TAGTATGGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTTCTCACCAGAGAGTC
	1391 DRD1,
1442	HisLeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeu CACTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTC GTGAATGGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAG
1502	GlyLeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsn GGCCTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAAC CCGGAGGACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTG
	1508 PSTI, 1513 TTH3I,
1562	TrpGlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGln TGGCAAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAA ACCGTTTTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTT
	1571 XHOI, 1592 NDEI,
1622	TyrLeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPhe TACTTGGCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTT ATGAACCGCCCGAACAGTTGCGACGGACCATTGGGGGCGGTAACGAAGTAACTACCGAAAA
	1649 BSTE2,
1682	ThrAlaAlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGly ACAGCTGCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGG TGTCGACGACAGTGGTCGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCC
	1683 ALWN1 PVU2,
1742	GlyTrpValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGly GGGTGGGTGGCTGCCCAGCTCGCCGCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGC CCCACCCACCGACGGGTCGAGCGGGGGGCCACGGCGATGACGGAAACACCCGCGACCG
	1800 ESP1,
1802	LeuAlaGlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAla TTAGCTGGCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGACATCCTTGCA AATCGACCGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGT
	1808 KAS1 NARI,

CCCATACCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAG

1862



662	TGCAATACGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTACCTTCACCATTGACACTATGACACTATGACACACAC
722	ThrileThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgArgArgArgArgArgArgArgArgArgArgArgArgA
782	GlyLysProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspGGGAAGCCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCGGCATGTTCGACCCCTTCGGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTC
	822 BGLI, 839 DRD1,
842	SerSerValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaTCGTCCGTCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTCACGCCCGCC
	887 SACI,
902	GluThrThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspGAGACTACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCTCTGATGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTG
	937 SMAI XMAI,
962	HisLeuGluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuCATCTTGAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCA
	991 STUI,
1022	SerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrVal TCCCAGACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTG AGGGTCTGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCAC
	1075 DRA3,
1082	CysAlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArg TGCGCTAGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGC ACGCGATCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACCTTCACAAACTAAGCG
1142	LeuLysProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsn CTCAAGCCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAAT GAGTTCGGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTA
	1156 NCOI,
1202	GlulleThrLeuThrHisProValThrLysTyrlleMetThrCysMetSerAlaAspLeu GAAATCACCCTGACGCACCCAGTCACCAAATACATCATGACATGCATG
	1236 BSPH1, 1240 DRD1, 1243 AVA3, 1251 EAG1 XMA3, 1256 DRD1,
	GluValValThrSerThrTrnValLeuValGlvGlvValLeuAlaAlaLeuAlaAlaTvr

CTCCAGCAGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGACGAAACCGGCGCATA

1262 GAGGTCGTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTAT

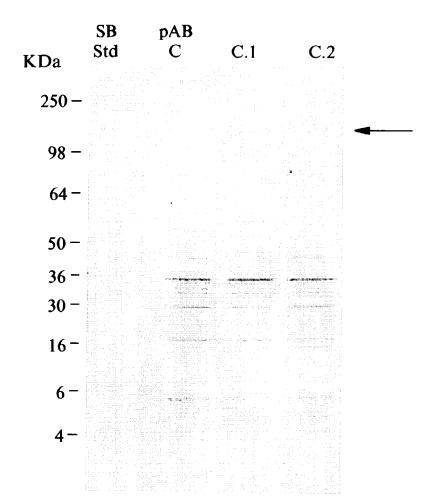


FIG. 12

3782	SerLysVallysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProProHisTCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCACACAGTTTCACTTCCGATCCGATCTCCTTCGAACGTCGGACTGCGGGGGTGTGAGGTTTTCACTTCCGATCGGACTGCGGGGGGTGTGAGGCATCTCCTTCGAACGTCGGACTGCGGGGGGTGTGAGGTTTCACTTCCGATCGGACTGCGGGGGGTGTGAGGTTTCACTTCGAACGTCGGACTGCGGGGGGTGTGAGGTTTCACTTCGAACGTCGGACTGCGGGGGTGTGAGGTTTTCACTTCGAACGTCGGACTGCGGGGGTGTGAGGTTTTCACTTCGAACGTCGGACTGCGGGGGTGTGAGGTTTTCACTTCGAACGTCGGACTGCGGGGGTGTGAGGTTTTCACTTCACTTCGAACGTCGGACTGCGGGGGGTGTGAGGTTTTCACTTCACTTCGAACGTCGGACTGCGGGGGGTGTGAGGTTTTCACTTC
	3816 HIND3,
3842	SerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAla TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAAGGCC AGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTCCGG
	3875 AAT2, 3890 BGLI,
3902	ValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIleAsp GTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAATAGAC CATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTATCTG
3962	ThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys ACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGTCGTAAG TGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCAGCATTC
4022	ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu CCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATGGCTTTG GGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTACCGAAAC
4082	TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr TACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCAATAC ATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAGGTTATG
4142	SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet TCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCCAATG AGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGGGGTTAC
	4160 ECORI,
1202	GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr GGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACG CCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAGGCATGC
	4229 DRD1, 4236 ALWN1,
262	GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer GAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAAGTCC CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGGTTCGGGCGCACCGGTAGTTCAGG
	4301 BGLI, 4308 BALI,
322	LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGlyCTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGCGGCGAGTGGCTCTCCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCCTCTTGACGCCG
	4345 APAI,
382	TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys TATCGCAGGTGCCGCGGGGGGGGGGTACTGACAACTAGCTGTGGTAACACCCTCACTTGC

ATAGCGTCCACGGCGCGCCGCATGACTGTTGATCGACACCATTGTGGGAGTGAACG

	GCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAAACCCGCGCCGGCCTGATATTGGG
	3143 ALWN1, 3164 EAG1 XMA3,
3182	ProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysProCCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTGCCCGGCGATCATCGTGGACACCAGGTACCGACGGGGGGCGATCACCTCTGTGGACACCAGGTACCGACGGGG
	3217 HGIE2, 3229 NCOI,
3242	LeuProProProLysSerProProValProProProArgLysLysArgThrValValLeuCTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTGGTCCTCGAAGGTGGAGGTTTCAGGGGAGGAGAAGCCGAGGAGCCTTCTTCGCCTGCCACCAGGACGAAGGTGGAGGTTTCAGGGGAGGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA
3302	ThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSerACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAGCTCGAGCTTGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCGTCGAGC
	3332 SACI, 3346 HIND3,
3362	SerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGlyTCAACTTCCGGCATTACGGCGACAATACGACATCCTCTGAGCCCGCCC
3422	CysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluProTGCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCTGGAGGGGGAGCCTACGGGGGGGG
	3437 EAM11051,
3482	GlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGlu GGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAACGCGGAG CCCCTAGGCCTAGAATCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTGCGCCTC
	3484 BAMHI, 3485 BSAB1, 3487 BSPE1,
3542	AspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAla GATGTCGTGTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTGCGCC CTACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCACGCGG
	3589 DRA3, 3600 SAC2,
3602	AlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsn GCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCACCACAAT CGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTGGTGTTA
	3611 ALWN1, 3655 PFLM1,
3662	LeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAsp TTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACATTTGAC AACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGTAAACTG
	3681 DRA3,
3722	ArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAla AGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAGCGGCG TCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTTCGTCGCCGC

CTCAAACTCACTCCAATAGCGGCCGCTGGCCAGCTGGACTTGTCCGGCTGGTTCACGGCT GAGTTTGAGTGAGGTTATCGCCGGCGACCGACCTGAACAGGCCGACCAAGTGCCGA

GlyTyrSerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrp
5222 GGCTACAGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCCGCTGGATCTGG
CCGATGTCGCCCCCTCTGTAAATAGTGTCGCACAGAGTACGGGCCGGGGCGACCTAGACC

5246 DRA3,

PheCysLeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgOP

TTTTGCCTACTCCTGCTTGCTGCAGGGGTAGGCATCTACCTCCCCAACCGATGAAGG
AAAACGGATGAGGACGACGACGTCCCCATCCGTAGATGGAGGGGGTTGGCTACTTCC

5301 PSTI, 5331 HGIE2,

5378 XBAI, 5390 SALI,

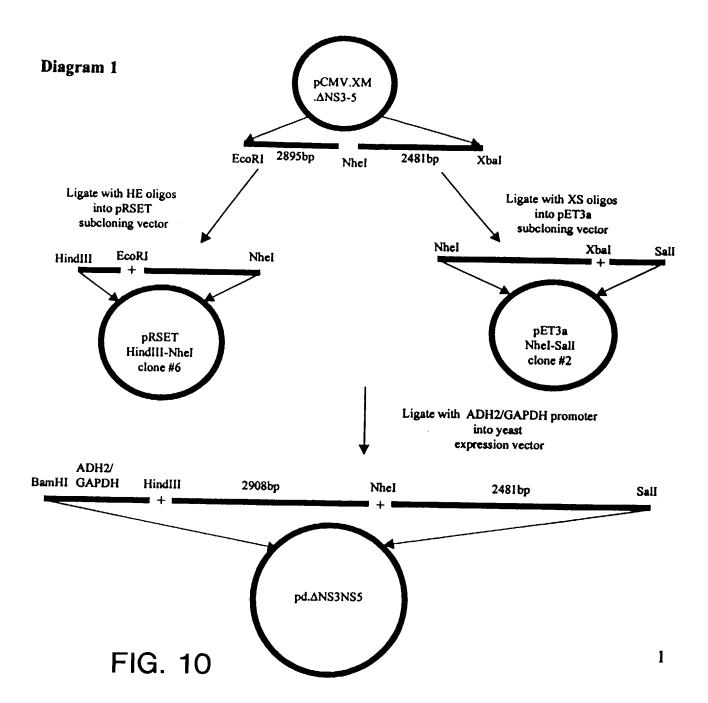
FIG. 11-Page 9

2	MetAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuVal AGCTTACAAAACAAATTCACCATGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTA TCGAATGTTTTGTTT
	1 HIND3, 21 NCOI, 30 NDEI, 58 SCAI,
62	LeuAsnProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGly CTCAACCCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGG GAGTTGGGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCC
122	IleAspProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyr ATCGATCCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTAC TAGCTAGGATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATG
	122 CLAI,
182	SerThrTyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIle TCCACCTACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGGCGCTTATGACATAATA AGGTGGATGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCCGCGAATACTGTATTAT
242	IleCysAspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuATTTGTGACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCACTGTCCTTTAAACACTGCTCACGGTGAGGTGCCTACGGTGTAGGTAG
302	AspGlnAlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlyGACCAAGCAGAGACTGCGGGGGGGGGGGGGGGGGGGGGG
	309 ALWN1,
362	SerValThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIle TCCGTCACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATC AGGCAGTGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAG
422	ProPheTyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePhe CCTTTTTACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTC GGAAAAATGCCGTTCCGATAGGGGGGAGCTTCATTAGTTCCCCCCCTCTGTAGAGTAGAAG
482	CysHisSerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsn TGTCATTCAAAGAAGAGTGCGACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAAT ACAGTAAGTTTCTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTA
542	AlaValAlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValGCCGTGGCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCCGGCACCGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGCTACAACAG
	556 SAC2, 566 DRD1,
602	ValValAlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerVallleAsp GTCGTGGCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCCATGACAC

 ${\tt CysAsnThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGlu}$

CAGCACCGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTG

621 BSPH1,



ACGCCGATAGCGTCCACGGCGCGCTCGCCGCATGACTGTTGATCG	CACCATTGTGGGA

- ThrCysTyrlleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMet
 4442 ACTTGCTACATCAAGGCCCGGGCAGCCTGTCGAGCCGCGGGCTCCCGAGGTCCTGACGTGCTAC
 TGAACGATGTAGTTCCGGGCCCGTCGGACAGCTCGGCGTCCCGAGGTCCTGACGTGGTAC
 - 4458 SMAI XMAI,
- LeuValCysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAla
 CTCGTGTGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCG
 GAGCACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGC
 - 4514 DRD1, 4517 TTH3I,
- AlaSerLeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspPro
 GCGAGCCTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCTGGGGACCCC
 CGCTCGGACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGGGACCCCTGGGG
- ProGlnProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAla

 4622 CCACAACCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCC
 GGTGTTGGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGG

 4643 SACI.
- HisAspGlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAla
 CACGACGGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCTCGCG
 GTGCTGCCGCGACCTTTCTCCCAGATGATGAGGGGCACTGGGATGTTGGGGGGGAGCGC
 - 4737 NRUI,
- ArgalaalaTrpGluThralaargHisThrProValAsnSerTrpLeuGlyAsnIleIle
 4742 AGAGCTGCGTGGGAGACAGCAAGACACTCCAGTCAATTCCTGGCTAGGCAACATAATC
 TCTCGACGCACCCTCTGTCGTTCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAG
- MetPheAlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeu
 4802 ATGTTTGCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTT
 TACAAACGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAA
 - 4812 PFLM1, 4813 DRA3,
- IleAlaArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSer
 4862 ATAGCCAGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCC
 TATCGGTCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGG
 - 4899 BGL2,
- IleGluProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSer
 4922 ATAGAACCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCA
 TATCTTGGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGT
 - 4960 NCOI,
- LeuHisSerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGly
 4982 CTCCACAGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACTTGGG
 GAGGTGTCAATGAGAGGTCCACTTTAGTTATCCCACCGGCGTACGGAGTCTTTTGAACCC
 - 5021 SPHI, 5041 KPNI,

- 3722 TTTGACAGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCA AAACTGTCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTTCGT ${\bf AlaAlaSerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrPro}$ GCGGCGTCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCC 3782 CGCCGCAGTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGG 3822 HIND3, ProHisSerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArg CCACACTCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGA 3842 GGTGTGAGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCT 3881 AAT2, 3896 BGLI, $Lys Ala Val Thr \verb|HisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThr \verb|Pro|| \\$ 3902 AAGGCCGTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCA TTCCGGCATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGT ${\tt IleAspThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGly}$ ATAGACACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGT TATCTGTGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCA ${\tt ArgLysProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMet}$ 4022 CGTAAGCCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATG GCATTCGGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTAC ${\tt AlaLeuTyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPhe}$ 4082 GCTTTGTACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTC CGAAACATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAG ${\tt GlnTyrSerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThr}$ 4142 CAATACTCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACC GTTATGAGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGG 4166 ECORI, ${\tt ProMetGlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIle}$ CCAATGGGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATC GGTTACCCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAG 4235 DRD1, 4242 ALWN1, ${\tt ArgThrGluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIle}$ 4262 CGTACGGAGGGAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATC GCATGCCTCCGCTTAGATGGTTACAACACTGGAGCTGGGGGGTTCGGGCGCACCGGTAG 4307 BGLI, 4314 BALI, ${\tt LysSerLeuThrGluArgLeuTyrValGlyGluProLeuThrAsnSerArgGlyGluAsn}$ 4322 AAGTCCCTCACCGAGAGGCTTTATGTTGGGGGGCCCTCTTACCAATTCAAGGGGGGAGAAC TTCAGGGAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCTCTTG 4351 APAI. ${\tt CysGlyTyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeu}$
 - FIG. 11-Page 7

4382 TGCGGCTATCGCAGGTGCCGCGCGAGCGGCGTACTGACAACTAGCTGTGGTAACACCCTC

3122	IleLeuArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyr ATCCTGCGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTAT TAGGACGCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGCCAAACCCGCGCCGGCCTGATA
	3149 ALWN1, 3170 EAG1 XMA3,
3182	AsnProProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGly AACCCCCCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGC TTGGGGGGCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCG
	3223 HGIE2, 3235 NCOI,
3242	CysProLeuProProProLysSerProProValProProProArgLysLysArgThrValTGCCCGCTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTGACGGCGAAGGAGGGGAGGGGGAGGCGAGCCTTCTTCGCCTGCCACACGGGGGGGG
3302	ValLeuThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlyGTCCTCACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCCAGGAGTGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCG
	3338 SACI, 3352 HIND3,
3362	SerSerSerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProAgCTCCTCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCGCCC
3422	SerGlyCysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyTCTGGCTGCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCTGGAGGGGAGACCTCCCCAGACCGACGACGACGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCC
	3443 EAM11051,
3482	GluProGlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsn GAGCCTGGGGATCCTGGACGGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAAC CTCGGACCCCTAGGCCTAGAATCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTG
	3490 BAMHI, 3491 BSAB1, 3493 BSPE1,
3542	AlaGluAspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrPro GCGGAGGATGTCGTGCTCCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCG CGCCTCCTACAGCACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGC
	3595 DRA3,
3602	CysAlaAlaGluGluGlnLysLeuProlleAsnAlaLeuSerAsnSerLeuLeuArgHis TGCGCCGCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCAC ACGCGCGCCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTG
	3606 SAC2, 3617 ALWN1, 3661 PFLM1,
3662	HisAsnLeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThr CACAATTTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACA GTGTTAAACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGT
	2607 0002

 ${\tt PheAspArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAla}$

5801	CAAGTCATTO GTTCAGTAA	TGAGAATAGT ACTCTTATCA	GTATGCGGCG	ACCGAGTTGC TGGCTCAACG	TCTTGCCCGG AGAACGGGCC
5851	CGTCAATACG	GGATAATACC	GCGCCACATA	GCAGAACTTT	AAAAGTGCTC
	GCAGTTATGC	CCTATTATGG	CGCGGTGTAT	CGTCTTGAAA	TTTTCACGAG
5901	ATCATTGGAA	AACGTTCTTC	GGGGCGAAAA	CTCTCAAGGA	TCTTACCGCT
	TAGTAACCTT	TTGCAAGAAG	CCCCGCTTTT	GAGAGTTCCT	AGAATGGCGA
5951	GTTGAGATCC	AGTTCGATGT	AACCCACTCG	TGCACCCAAC	TGATCTTCAG
	CAACTCTAGG	TCAAGCTACA	TTGGGTGAGC	ACGTGGGTTG	ACTAGAAGTC
6001	CATCTTTTAC	TTTCACCAGC	GTTTCTGGGT	GAGCAAAAAC	AGGAAGGCAA
	GTAGAAAATG	AAAGTGGTCG	CAAAGACCCA	CTCGTTTTTG	TCCTTCCGTT
6051		AAAAGGGAAT TTTTCCCTTA	AAGGGCGACA TTCCCGCTGT	CGGAAATGTT GCCTTTACAA	GAATACTCAT CTTATGAGTA
6101	ACTCTTCCTT	TTTCAATATT	ATTGAAGCAT	TTATCAGGGT	TATTGTCTCA
	TGAGAAGGAA	AAAGTTATAA	TAACTTCGTA	AATAGTCCCA	ATAACAGAGT
6151	TGAGCGGATA	CATATTTGAA	TGTATTTAGA	AAAATAAACA	AATAGGGGTT
	ACTCGCCTAT	GTATAAACTT	ACATAAATCT	TTTTATTTGT	TTATCCCCAA
6201	CCGCGCACAT	TTCCCCGAAA	AGTGCCACCT	GACGTCTAAG	AAACCATTAT
	GGCGCGTGTA	AAGGGGCTTT	TCACGGTGGA	CTGCAGATTC	TTTGGTAATA
6251	TATCATGACA	TTAACCTATA	AAAATAGGCG	TATCACGAGG	CCCTTTCGTC
	ATAGTACTGT	AATTGGATAT	TTTTATCCGC	ATAGTGCTCC	GGGAAAGCAG

FIG. 9-Page 8

4851		A GGTATGTAG	G CGGTGCTAC	A GAGTTCTTG	AGTGGTGGCC
	TCGTCTCGC	T CCATACATC	C GCCACGATG	CTCAAGAACT	TCACCACCGG
4901		C TACACTAGAI G ATGTGATCT	A GGACAGTAT: I CCTGTCATAI	TGGTATCTGC	G GCTCTGCTGA G CGAGACGACT
4951		C CTTCGGAAAI G GAAGCCTTT	A AGAGTTGGTA T TCTCAACCA	A GCTCTTGATO	C CGGCAAACAA G GCCGTTTGTT
5001		G GTAGCGGTGG C CATCGCCACG	TTTTTTTGTT	TGCAAGCAGO ACGTTCGTCG	AGATTACGCG TCTAATGCGC
5051		A GGATCTCAAC I CCTAGAGTTC	AAGATCCTTT TTCTAGGAAA	GATCTTTTCT CTAGAAAAGA	ACGGGGTCTG TGCCCCAGAC
5101		GAACGAAAAC CTTGCTTTTG	TCACGTTAAG AGTGCAATTC	GGATTTTGGT CCTAAAACCA	CATGAGATTA GTACTCTAAT
5151		A TCTTCACCTA C AGAAGTGGAT	GATCCTTTTA CTAGGAAAAT	AATTAAAAAT TTAATTTTA	GAAGTTTTAA CTTCAAAATT
5201		AGTATATATG TCATATATAC	AGTAAACTTG TCATTTGAAC	GTCTGACAGT CAGACTGTCA	TACCAATGCT ATGGTTACGA
5251		GGCACCTATC CCGTGGATAG	TCAGCGATCT AGTCGCTAGA	GTCTATTTCG CAGATAAAGC	TTCATCCATA AAGTAGGTAT
5301		TCCCCGTCGT AGGGGCAGCA	GTAGATAACT CATCTATTGA	ACGATACGGG TGCTATGCCC	AGGGCTTACC TCCCGAATGG
5351	ATCTGGCCCC TAGACCGGGG	AGTGCTGCAA TCACGACGTT	TGATACCGCG ACTATGGCGC	AGACCCACGC TCTGGGTGCG	TCACCGGCTC AGTGGCCGAG
5401	CAGATTTATC GTCTAAATAG	AGCAATAAAC TCGTTATTTG	CAGCCAGCCG GTCGGTCGGC	GAAGGGCCGA CTTCCCGGCT	GCGCAGAAGT CGCGTCTTCA
5451	GGTCCTGCAA CCAGGACGTT	CTTTATCCGC GAAATAGGCG	CTCCATCCAG GAGGTAGGTC	TCTATTAATT AGATAATTAA	GTTGCCGGGA CAACGGCCCT
5501	AGCTAGAGTA TCGATCTCAT	AGTAGTTCGC TCATCAAGCG	CAGTTAATAG GTCAATTATC	TTTGCGCAAC AAACGCGTTG	GTTGTTGCCA CAACAACGGT
5551	TTGCTACAGG AACGATGTCC	CATCGTGGTG GTAGCACCAC	TCACGCTCGT AGTGCGAGCA	CGTTTGGTAT GCAAACCATA	GGCTTCATTC CCGAAGTAAG
5601	AGCTCCGGTT TCGAGGCCAA	CCCAACGATC GGGTTGCTAG	AAGGCGAGTT TTCCGCTCAA	ACATGATCCC TGTACTAGGG	CCATGTTGTG GGTACAACAC
5651	CAAAAAAGCG GTTTTTTCGC	GTTAGCTCCT CAATCGAGGA	TCGGTCCTCC AGCCAGGAGG	GATCGTTGTC CTAGCAACAG	AGAAGTAAGT TCTTCATTCA
5701	TGGCCGCAGT ACCGGCGTCA	GTTATCACTC CAATAGTGAG	ATGGTTATGG TACCAATACC	CAGCACTGCA GTCGTGACGT	TAATTCTCTT ATTAAGAGAA
5 751	ACTGTCATGC TGACAGTACG	CATCCGTAAG GTAGGCATTC	ATGCTTTTCT TACGAAAAGA	GTGACTGGTG CACTGACCAC	AGTACTCAAC TCATGAGTTG

		.	_	_	CIVI V					
39	951	GCG1GG1C	AT AGT	GGGCAG (GTCG'	アアヤスコ	S G K CCGGGAAC GGCCCTTC	200	CCCAAT	יד ביי
40	+2 001	CCTGACAG	GG AAG	CCTCTA	CCGAC	ACTTO	D E N GATGAGA1 CTACTCTA	CC	ABGAGT	- -
		BamHI	Mlul	[- ·		·	
40	51	GGATCCAC	TA CGCC	TTAGAG	CTCGC GAGCG	TGATO ACTAG	AGCCTCGA TCGGAGCT	CT GA	GTGCCT CACGGA	TCT! AGA1
41	01	GTTGCCAG CAACGGTC	CC ATCT GG TAGA	GTTGTT CAACAA	TGCCC	CTCCC	CCGTGCCT GGCACGGA	TC AG	CTTGAC GAACTG	CCT (
41	51	GAAGGTGC CTTCCACG	CA CTCC GT GAGG	CACTGT GTGACA	CCTTT	CCTAA GGATT	TAAAATGA ATTTTACT	GG ,	AAATTG TTTAAC	CATO
42	01	GCATTGTC: CGTAACAG	IG AGTA AC TCAT	GGTGTC CCACAG	ATTCT TAAGA	ATTCT TAAGA	GGGGGGTG CCCCCAC	GG (GTGGGG CACCCC	CAGG GTCC
42	51	ACAGCAAGO TGTCGTTCO	GG GGAG	GATTGG CTAACC	GAAGA CTTCT	CAATA GTTAT	GCAGGCATO CGTCCGTA	GC :	rgggga(ACCCCT(GCTC CGAG
43		TTCCGCTT(AAGGCGAA(CC TCGC	TCACTG AGTGAC	ACTCG TGAGC	CTGCG GACGC	CTCGGTCG'	TT (CGGCTGC	CGGC GCCG
43:	-	GAGCGGTAT CTCGCCATA	C AGCTO	CACTCA STGAGT	AAGGC0 TTCCG0	GGTAA CCATT	TACGGTTA:	 IC (CACAGAA	ATCA TAGT
44(_	GGGGATAAC CCCCTATTG	G CAGG	AAAGAA TTTCTT	CATGT(GAGCA CTCGT	AAAGGCCAC TTTCCGGTC	GC A	AAAGGC	CAG GTC
445		GAACCGTAA CTTGGCATT	A AAGGO	CGCGT GCGCA	TGCTG(GCAA	TTTCCATAG AAAGGTATC	G C	TCCGCC	CCC GGG
450	01 (CTGACGAGC GACTGCTCG	A TCACA T AGTGT	AAAAT	CGACGO	TCAA AGTT	GTCAGAGGT CAGTCTCCA	'G G	CGAAAC	CCG GGC
155	1 7	ACAGGACTA GTCCTGAT	T AAAGA A TTTCT	TACCA	GGCGT1 CCGCAA	TCCC AGGG	CCTGGAAGC GGACCTTCG	T C	CCTCGT GGAGCA	GCG CGC
60	1 0	TCTCCTGT AGAGGACA	T CCGAC A GGCTG	CCTGC GGACG	CGCTTA GCGAAT	CCGG	ATACCTGTC TATGGACAG	C G	CCTTTC GGAAAG	TCC AGG
65	1 C	TTCGGGAA(AAGCCCTT	G CGTGG GCACC	CGCTT GCGAA	TCTCAA AGAGTT	TGCT (CACGCTGTA GTGCGACAT	G G	TATCTC: ATAGAG:	AGT TCA
70	1 T	CGGTGTAG(GCCACATC(G TCGTT	CGCTC (CAAGCT GTTCGA	GGGC 1	TGTGTGCAC ACACACGTG	G A	ACCCCC(CGT GCA
75	1 T	CAGCCCGA(GTCGGGCT(CGCTG	CGCCT C	TATCCG ATAGGC	GTAA (CATT (CTATCGTCT' SATAGCAGA	I GA	AGTCCAJ CAGGTT	ACC rgg
80:	G G	GGTAAGACA CCATTCTGT	CGACT	TATCG (CACTG	GCAG (CAGCCACTG(GTCGGTGAC(TA C	ACAGGA TGTCC1	TTA

2486 ASE1, 2503 APAI,

ProAlaProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIle CCTGCGCCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATA GGACGCGGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTAT

2559 PSTI,

- ArgGlnValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysPro
 AGGCAGGTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCG
 TCCGTCCACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGC
 2600 DRA3.
- CysGlnValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPhe
 TGCCAGGTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTT
 ACGGTCCAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAA
- AlaProProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGlu 2702 GCGCCCCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAA CGCGGGGGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTT
- TyrProValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSer
 TACCCGGTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCC
 ATGGGCCATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGG

 2763 HGIE2, 2815 AAT2,
- MetLeuThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGly
 ATGCTCACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGA
 TACGAGTGACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCCGCTTCCAACCGCTCCCCT

 2856 EAG1 XMA3.
- SerProProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAla
 TCACCCCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCA
 AGTGGGGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGT

 2895 BALI, 2909 NHEI,
- ThrCysThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrp
 ACTTGCACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGG
 TGAACGTGGCGATTGGTACTGAGGGGACTACGACTCCGAGTATCTCCGGTTGGAGGATACC

2972 ESP1, 2975 SACI,

3102 BGL2.

- ArgGlngIuMētGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeu 3002 AGGCAGGAGATGGGCGAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTG TCCGTCCTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGAC

FIG. 11-Page 5

- +2 G D F D S V I D C N T C V T Q T V
 3251 GGCGACTTCG ACTCGGTGAT AGACTGCAAT ACGTGTGTCA CCCAGACAGT
 CCGCTGAAGC TGAGCCACTA TCTGACGTTA TGCACACAGT GGGTCTGTCA
- +2 D F S L D P T F T I E T I T L P
 3301 CGATTTCAGC CTTGACCCTA CCTTCACCAT TGAGACAATC ACGCTCCCCC
 GCTAAAGTCG GAACTGGGAT GGAAGTGGTA ACTCTGTTAG TGCGAGGGGG
- +2 Q D A V S R T Q R R G R T G R G K
 3351 AAGATGCTGT CTCCCGCACT CAACGTCGGG GCAGGACTGG CAGGGGGAAG
 TTCTACGAGA GAGGGCGTGA GTTGCAGCCC CGTCCTGACC GTCCCCCTTC
- +2 P G I Y R F V A P G E R P S G M F 3401 CCAGGCATCT ACAGATTTGT GGCACCGGGG GAGCGCCCCT CCGGCATGTT GGTCCGTAGA TGTCTAAACA CCGTGGCCCC CTCGCGGGGA GGCCGTACAA
- +2 D S S V L C E C Y D A G C A W Y
 3451 CGACTCGTCC GTCCTCTGTG AGTGCTATGA CGCAGGCTGT GCTTGGTATG
 GCTGAGCAGG CAGGAGACAC TCACGATACT GCGTCCGACA CGAACCATAC
- +2 E L T P A E T T V R L R A Y M N T

 3501 AGCTCACGCC CGCCGAGACT ACAGTTAGGC TACGAGCGTA CATGAACACC
 TCGAGTGCGG GCGGCTCTGA TGTCAATCCG ATGCTCGCAT GTACTTGTGG
- +2 P G L P V C Q D H L E F W E G V F 3551 CCGGGGCTTC CCGTGTGCCA GGACCATCTT GAATTTTGGG AGGGCGTCTT GGCCCCGAAG GGCACACGGT CCTGGTAGAA CTTAAAACCC TCCCGCAGAA
 - +2 T G L T H I D A H F L S Q T K Q
 StuI
- 3601 TACAGGCCTC ACTCATATAG ATGCCCACTT TCTATCCCAG ACAAAGCAGA ATGTCCGGAG TGAGTATATC TACGGGTGAA AGATAGGGTC TGTTTCGTCT
- +2 S G E N L P Y L V A Y Q A T V C A
 3651 GTGGGGAGAA CCTTCCTTAC CTGGTAGCGT ACCAAGCCAC CGTGTGCGCT
 CACCCCTCTT GGAAGGAATG GACCATCGCA TGGTTCGGTG GCACACGCGA
- +2 R A Q A P P P S W D Q M W K C L I 3701 AGGGCTCAAG CCCCTCCCCC ATCGTGGGAC CAGATGTGGA AGTGTTTGAT TCCCGAGTTC GGGGAGGGGG TAGCACCCTG GTCTACACCCT TCACAAACTA
- +2 R L K P T L H G P T P L L Y R L
 3751 TCGCCTCAAG CCCACCCTCC ATGGGCCAAC ACCCCTGCTA TACAGACTGG
 AGCGGAGTTC GGGTGGGAGG TACCCGGTTG TGGGGACGAT ATGTCTGACC
- +2 G A V Q N E I T L T H P V T K Y I 3801 GCGCTGTTCA GAATGAAATC ACCCTGACGC ACCCAGTCAC CAAATACATC CGCGACAAGT CTTACTTTAG TGGGACTGCG TGGGTCAGTG GTTTATGTAG
- +2 M T C M S A D L E V V T S T W V L 3851 ATGACATGCA TGTCGGCCGA CCTGGAGGTC GTCACGAGCA CCTGGGTGCT TACTGTACGT ACAGCCGGCT GGACCTCCAG CAGTGCTCGT GGACCCACGA
- +2 V G G V L A A L A A Y C L S T G
 3901 CGTTGGCGGC GTCCTGGCTG CTTTGGCCGC GTATTGCCTG TCAACAGGCT
 GCAACCGCCG CAGGACCGAC GAAACCGGCG CATAACGGAC AGTTGTCCGA

- +2 N S S P P V V P Q S F Q V A H L
 2551 TAACTCCTCT CCACCAGTAG TGCCCCAGAG CTTCCAGGTG GCTCACCTCC
 ATTGAGGAGA GGTGGTCATC ACGGGGTCTC GAAGGTCCAC CGAGTGGAGG
- +2 H A P T G S G K S T K V P A A Y A
 2601 ATGCTCCCAC AGGCAGCGGC AAAAGCACCA AGGTCCCGGC TGCATATGCA
 TACGAGGGTG TCCGTCGCCG TTTTCGTGGT TCCAGGGCCG ACGTATACGT
- +2 A Q G Y K V L V L N P S V A A T L
 2651 GCTCAGGGCT ATAAGGTGCT AGTACTCAAC CCCTCTGTTG CTGCAACACT
 CGAGTCCCGA TATTCCACGA TCATGAGTTG GGGAGACAAC GACGTTGTGA
- +2 G F G A Y M S K A H G I D P N I 2701 GGGCTTTGGT GCTTACATGT CCAAGGCTCA TGGGATCGAT CCTAACATCA CCCGAAACCA CGAATGTACA GGTTCCGAGT ACCCTAGCTA GGATTGTAGT
- +2 R T G V R T I T T G S P I T Y S T
 2751 GGACCGGGGT GAGAACAATT ACCACTGGCA GCCCCATCAC GTACTCCACC
 CCTGGCCCCA CTCTTGTTAA TGGTGACCGT CGGGGTAGTG CATGAGGTGG
- +2 Y G K F L A D G G C S G G A Y D I 2801 TACGGCAAGT TCCTTGCCGA CGGCGGGTGC TCGGGGGGGC CTTATGACAT ATGCCGTTCA AGGAACGGCT GCCGCCCACG AGCCCCCCGC GAATACTGTA
- +2 I I C D E C H S T D A T S I L G 2851 AATAATTTGT GACGAGTGCC ACTCCACGGA TGCCACATCC ATCTTGGGCA TTATTAAACA CTGCTCACGG TGAGGTGCCT ACGGTGTAGG TAGAACCCGT
- +2 I G T V L D Q A E T A G A R L V V 2901 TTGGCACTGT CCTTGACCAA GCAGAGACTG CGGGGGCGAG ACTGGTTGTG AACCGTGACA GGAACTGGTT CGTCTCTGAC GCCCCCGCTC TGACCAACAC
- +2 L A T A T P P G S V T V P H P N I 2951 CTCGCCACCG CCACCCCTCC GGGCTCCGTC ACTGTGCCCC ATCCCAACAT GAGCGGTGGC GGTGGGGAGG CCCGAGGCAG TGACACGGGG TAGGGTTGTA
- +2 E E V A L S T T G E I P F Y G K
 3001 CGAGGAGGTT GCTCTGTCCA CCACCGGAGA GATCCCTTTT TACGGCAAGG
 GCTCCTCCAA CGAGACAGGT GGTGGCCTCT CTAGGGAAAA ATGCCGTTCC
- +2 A I P L E V I K G G R H L I F C H
 3051 CTATCCCCCT CGAAGTAATC AAGGGGGGGA GACATCTCAT CTTCTGTCAT
 GATAGGGGGA GCTTCATTAG TTCCCCCCCT CTGTAGAGTA GAAGACAGTA
- +2 S K K K C D E L A A K L V A L G I 3101 TCAAAGAAGA AGTGCGACGA ACTCGCCGCA AAGCTGGTCG CATTGGGCAT AGTTTCTTCT TCACGCTGCT TGAGCGGCGT TTCGACCAGC GTAACCCGTA
- +2 N A V A Y Y R G L D V S V I P T 3151 CAATGCCGTG GCCTACTACC GCGGTCTTGA CGTGTCCGTC ATCCCGACCA GTTACGGCAC CGGATGATGG CGCCAGAACT GCACAGGCAG TAGGGCTGGT
- +2 S G D V V V V A T D A L M T G Y T
 3201 GCGGCGATGT TGTCGTCGTG GCAACCGATG CCCTCATGAC CGCCTATACC
 CGCCGCTACA ACAGCAGCAC CGTTGGCTAC GGGAGTACTG GCCGATATGG

TTAACGGTGG AGGGCAGTGT AGTCTGAGCA GTACTCGTTG CTGCCGCGCG AATTGCCACC TCCCGTCACA TCAGACTCGT CATGAGCAAC GACGGCGCGC 1901 CGCCACCAGA CATAATAGCT GACAGACTAA CAGACTGTTC CTTTCCATGG GCGGTGGTCT GTATTATCGA CTGTCTGATT GTCTGACAAG GAAAGGTACC +2 MAP **EcoRI** 1951 GTCTTTTCTG CAGTCACCGT CGTCGACCTA AGAATTCACC ATGGCGCCCA CAGAAAAGAC GTCAGTGGCA GCAGCTGGAT TCTTAAGTGG TACCGCGGGT A Q O TRGL LGC IIT 2001 TCACGGCGTA CGCCCAGCAG ACAAGGGGCC TCCTAGGGTG CATAATCACC AGTGCCGCAT GCGGGTCGTC TGTTCCCCGG AGGATCCCAC GTATTAGTGG +2 S L T G RDK NOV EGEV 2051 AGCCTAACTG GCCGGGACAA AAACCAAGTG GAGGGTGAGG TCCAGATTGT TCGGATTGAC CGGCCCTGTT TTTGGTTCAC CTCCCACTCC AGGTCTAACA STA +2 AQTF LAT CIN G V C 2101 GTCAACTGCT GCCCAAACCT TCCTGGCAAC GTGCATCAAT GGGGTGTGCT CAGTTGACGA CGGGTTTGGA AGGACCGTTG CACGTAGTTA CCCCACACGA +2 W T V Y H G A GTRT I A S 2151 GGACTGTCTA CCACGGGGCC GGAACGAGGA CCATCGCGTC ACCCAAGGGT CCTGACAGAT GGTGCCCCGG CCTTGCTCCT GGTAGCGCAG TGGGTTCCCA -2 P V I Q MYT N V D QDLV 2201 CCTGTCATCC AGATGTATAC CAATGTAGAC CAAGACCTTG TGGGCTGGCC GGACAGTAGG TCTACATATG GTTACATCTG GTTCTGGAAC ACCCGACCGG G T R S A S O LTP CTC G S S 2251 CGCTTCGCAA GGTACCCGCT CATTGACACC CTGCACTTGC GGCTCCTCGG GCGAAGCGTT CCATGGGCGA GTAACTGTGG GACGTGAACG CCGAGGAGCC +2 D L Y L VTR HADV 2301 ACCTTTACCT GGTCACGAGG CACGCCGATG TCATTCCCGT GCGCCGGCGG TGGAAATGGA CCAGTGCTCC GTGCGGCTAC AGTAAGGGCA CGCGGCCGCC +2 G D S R G S L LSP RPIS 2351 GGTGATAGCA GGGGCAGCCT GCTGTCGCCC CGGCCCATTT CCTACTTGAA CCACTATCGT CCCCGTCGGA CGACAGCGGG GCCGGGTAAA GGATGAACTT GGPL LCP AGH AVG 2401 AGGCTCCTCG GGGGGTCCGC TGTTGTGCCC CGCGGGGCAC GCCGTGGGCA TCCGAGGAGC CCCCCAGGCG ACAACACGGG GCGCCCCGTG CGGCACCCGT +2 I F R A A V C TRGV AKA TATTTAGGGC CGCGGTGTGC ACCCGTGGAG TGGCTAAGGC GGTGGACTTT ATAAATCCCG GCGCCACACG TGGGCACCTC ACCGATTCCG CCACCTGAAA +2 I P V E NLE TTM RSPV 2501 ATCCCTGTGG AGAACCTAGA GACAACCATG AGGTCCCCGG TGTTCACGGA

TAGGGACACC TCTTGGATCT CTGTTGGTAC TCCAGGGGCC ACAAGTGCCT

	CTCAACAACA	ATTCTGATAA TAAGACTATT	GAGTCAGAGG CTCAGTCTCC	TAACTCCCGT S ATTGAGGGCA	TGCGGTGCTG ACGCCACGAC
	CCIGCGICIA	CCTTCTGAAT	TCCGTCGCCG	AGAAGAAGAT (TCTTCTTCTA	CGTCCGTCGA
	CCGCCATCCC	ATACACAGAC	TTTTACTCGA	CGGAGATTGG GCCTCTAACC	CGAGCGTGGA
1651	CTTAGGCACA GAATCCGTGT	GCACAATGCC CGTGTTACGG	CACCACCACC GTGGTGGTGG	AGTGTGCCGC TCACACGGCG	ACAAGGCCGT TGTTCCGGCA
1601	GCGGCTCATG CGCCGAGTAC	GTCGCTCGGC CAGCGAGCCG	AGCTCCTTGC TCGAGGAACG	TCCTAACAGT AGGATTGTCA	GGAGGCCAGA CCTCCGGTCT
1551	CTCCGGTAGC GAGGCCATCG	GGCGGAGCTT CCGCCTCGAA	CCACATCCGA GGTGTAGGCT	GCCCTGGTCC CGGGACCAGG	CATCCGTCCA GTAGGCAGGT
1501	TAGCGTGGGA ATCGCACCCT	TCTCCGACAT AGAGGCTGTA	CTCGGGTACG GAGCCCATGC	TGTTCCGGAC ACAAGGCCTG	ATGGGCTCTT TACCCGAGAA
1451	TTCACATATA AAGTGTATAT	CAACAACGCC GTTGTTGCGG	GTCCCCGTG CAGGGGGCAC	CCCGCAGTTT GGGCGTCAAA	TTATTAAACA AATAATTTGT
1401	GACACGGACT CTGTGCCTGA	CTGTATTTT GACATAAAAA	ACAGGATGGG TGTCCTACCC	GTCCATTTAT CAGGTAAATA	TATTTACAAA ATAAATGTTT
1351	CCACAACTA? GGTGTTGATA	CTCTATTGGC	TATATGCCAA ATATACGGTT	TACTCTGTCC ATGAGACAGG	TTCAGAGACT AAGTCTCTGA
1301		GACGATACTI CTGCTATGA	TCCATTACTA A AGGTAATGAT	ATCCATAACA TAGGTATTGT	TGGCTCTTTG ACCGAGAAAC
1251		TAGCCTATAC A ATCGGATATC	G GTGTGGGTTA CACACCCAAT	TTGACCATTA AACTGGTAAT	TTGACCACTC AACTGGTGAG
1201		G CTTGGGGCCT C GAACCCCGGI	TATACACCCCC	GCTCCTTATG GCGAGGAATAC	CTATAGGTGA GATATCCACT
1151		G ACTCTATAGO C TGAGATATCO	G CACACCCCTI	TGGCTCTTAT ACCGAGAATA	GCATGCTATA CGTACGATAT
1101		C ATTGGAACGG G TAACCTTGCG	C GGATTCCCCC G CCTAAGGGGC	G TGCCAAGAGT C ACGGTTCTCA	GACGTAAGTA CTGCATTCAT
1051		C TCCATAGAA G AGGTATCTT	G ACACCGGGAG C TGTGGCCCTG	C CGATCCAGCC G GCTAGGTCGG	TCCGCGGCCG AGGCGCCGGC
1001		G TTTAGTGAA C AAATCACTT	C CGTCAGATCO G GCAGTCTAGO	G CCTGGAGACG GGACCTCTGC	CCATCCACGC GGTAGGTGCG
951	CCCGTTGAC GGGCAACTG	CG CAAATGGGC CC GTTTACCCG	G GTAGGCGTG	T ACGGTGGGAG A TGCCACCCTC	GTCTATATAA CAGATATATT
901		CC AAAATCAAC GG TTTTAGTTG	G GGACTTTCC C CCTGAAAGG	A AAATGTCGTA T TTTACAGCA1	A ATAACCCCGC TATTGGGGCG

51	ACTCACGGGG TGAGTGCCCC	ATTTCCAAGT	CTCCACCCCA	TTGACGTCAA	TGGGAGTTTG
01	GIACCACTAC	GCCAAAACCG	TCATGTGGTT	TGGGCGTGGA ACCCGCACCT	ATCGCCAAAC
751	CGGGACTTTC GCCCTGAAAG	CTACTTGGCA GATGAACCGT	GTACATCTAC CATGTAGATG	GTATTAGTCA CATAATCAGT	TCGCTATTAC AGCGATAATG
701		TAAATGGCCC ATTTACCGGG	GCCTGGCATT CGGACCGTAA	ATGCCCAGTA TACGGGTCAT	CATGACCTTA GTACTGGAAT
651	CTTGGCAGTA GAACCGTCAT	CATCAAGTGT GTAGTTCACA	ATCATATGCC TAGTATACGG	AAGTCCGCCC TTCAGGCGGG	CCTATTGACG GGATAACTGC
601	GGGACTTTCC CCCTGAAAGG	ATTGACGTCA TAACTGCAGT	ATGGGTGGAG TACCCACCTC	TATTTACGGT ATAAATGCCA	AAACTGCCCA TTTGACGGGT
551	CCCGCCCATT GGGCGGGTAA	GACGTCAATA CTGCAGTTAT	ATGACGTATG TACTGCATAC	TTCCCATAGT AAGGGTATCA	AACGCCAATA TTGCGGTTAT
501	CGTTACATAA GCAATGTATT	CTTACGGTAA GAATGCCATT	ATGGCCCGCC TACCGGGCGG	TGGCTGACCG ACCGACTGGC	CCCAACGACC GGGTTGCTGG
451	TAGTAATCAA ATCATTAGTT	TTACGGGGTC AATGCCCCAG	ATTAGTTCAT TAATCAAGTA	AGCCCATATA TCGGGTATAT	TGGAGTTCCG ACCTCAAGGC
401	CATGTCCAA1 GTACAGGTTA	TACTGGCGGT	TGTTGACATT ACAACTGTAA	GATTATTGAC CTAATAACTG	TAGTTATTAA ATCAATAATT
351	GCCATTGCA1 CGGTAACGTA	ACGTTGTATO	TATATCATAA ATATAGTATT	TATGTACATT ATACATGTAA	TATATTGGCT ATATAACCGA
301		AATGGGCGG	A ACTGGGCGGG	GAGGGAATTA CTCCCTTAAT	TTGGCTATTO
251		GGCCTCGGCG GCCGGAGCCGG	C TCTGCATAAA G AGACGTATTI	TAAAAAAAA TAATTATTTTA	TAGTCAGCCA ATCAGTCGGT
201	AAAGCCTAGG TTTCGGATCG	G CCTCCAAAA G GGAGGTTTT	A AGCCTCCTCA T TCGGAGGAGA	A CTACTTCTGG	AATAGCTCAC TTATCGAGTC
		tuI	T GACTCTCAC	G TGGTATACT1	CGAAAAACG
151	CGGCATCAG	AGTEGEECA A GEAGATTGT	C AACCGCCCA ——————————————————————————————	AGCCCCGACC	GAATTGATA
101	TCAGGGCGC	G TCAGCGGGT	G TTGGCGGGT	TCGGGGCTG	
51	GAGACGGTC	A CAGCTTGTC	T GTAAGCGGA	T GCCGGGAGCA A CGGCCCTCG	GACAAGCCC
1	TCGCGCGTT AGCGCGCAA	T CGGTGATGA A GCCACTACT	C GGTGAAAAC G CCACTTTG	C TCTGACACA? G AGACTGTGT	r GCAGCTCCC A CGTCGAGGG

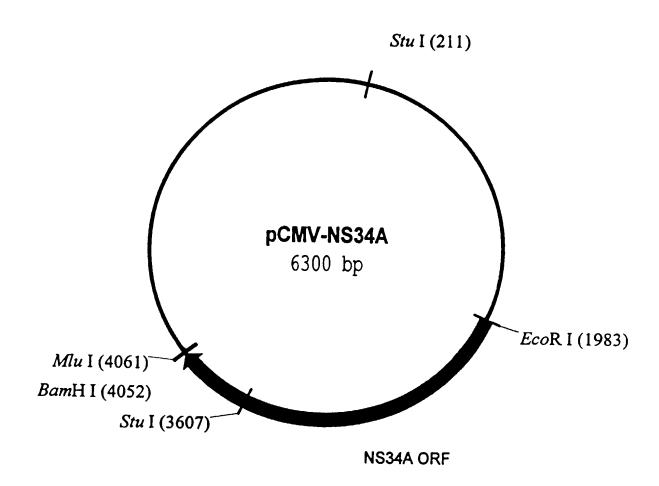


FIG. 8

pCMV-II

3521	TTGCCATTGC AACGGTAACG	TACAGGCATC	GTGGTGTCAC CACCACAGTG		PCMV-II GCTCGTCGTT TGGTATGGCT CGAGCAGCAA ACCATACCGA	TCATTCAGCT AGTAAGTCGA	CCGGTTCCCA GGCCAAGGGT	ACGATCAAGG TGCTAGTTCC
3601	CGAGTTACAT GCTCAATGTA	GATCCCCCAT CTAGGGGGGTA	GTTGTGCAAA	AAAGCGGTTA TTTCGCCAAT	GCTCCTTCGG	TCCTCCGATC AGGAGGCTAG	GTTGTCAGAA	GTAAGTTGGC
3681	CGCAGTGTTA GCGTCACAAT	TCACTCATGG AGTGAGTACC	TTATGGCAGC	ACTGCATAAT TGACGTATTA	TCTCTTACTG	TCATGCCATC AGTACGGTAG	CGTAAGATGC	TTTTCTGTGA
3761	CTGGTGAGTA GACCACTCAT	CTCAACCAAG GAGTTGGTTC	TCATTCTGAG AGTAAGACTC	AATAGTGTAT TTATCACATA	GCGGCGACCG	AGTTGCTCTT TCAACGAGAA	GCCCGGCGTC	AATACGGGAT TTATGCCCTA
3841	AATACCGCGC TTATGGCGCG	CACATAGCAG GTGTATCGTC	AACTTTAAAA TTGAAATTTT	GTGCTCATCA	TTGGAAAACG AACCTTTTGC	TTCTTCGGGG	CGAAAACTCT GCTTTTGAGA	CAAGGATCTT
3921	ACCGCTGTTG TGGCGACAAC	AGATCCAGTT TCTAGGTCAA	CGATGTAACC GCTACATTGG	CACTCGTGCA GTGAGCACGT	CCCAACTGAT GGGTTGACTA	CTTCAGCATC	TTTTACTTTC AAAATGAAAG	ACCAGCGTTT TGGTCGCAAA
4001	CTGGGTGAGC GACCCACTCG	AAAAACAGGA , TTTTTGTCCT	AGGCAAAATG TCCGTTTTAC	CCGCAAAAAA	GGGAATAAGG	GCGACACGGA	AATGTTGAAT TTACAACTTA	ACTCATACTC TGAGTATGAG
4081	TTCCTTTTTC AAGGAAAAG	AATATTATTG /	AAGCATTTAT TTCGTAAATA	CAGGGTTATT GTCCCAATAA	GTCTCATGAG	CGGATACATA GCCTATGTAT	TTTGAATGTA AAACTTACAT	TTTAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
4161	TAAACAAATA ATTTGTTTAT	GGGGTTCCGC (GCACATTTCC CGTGTAAAGG	CCGAAAAGTG GCCTTTTCAC	CCACCTGACG	TCTAAGAAAC (AGATTCTTTG (CATTATTATC	ATGACATTAA TACTGTAATT
4241	CCTATAAAAA GGATATTTT	TAGGCGTATC A	ACGAGGCCCT TGCTCCGGGA	TTCGTC				

FIG. 7-Page 6

pCMV-II

2801	TGGCAGCAGC	CACTGGTAAC GTGACCATTG	AGGATTAGCA TCCTAATCGT	GAGCGAGGTA CTCGCTCCA1	TGTAGGCGGT	GCTACAGAGT TCTTGAAGTG CGATGTCTCA AGAACTTCAC	TCTTGAAGTG AGAACTTCAC	GTGGCCTAAC CACCGGATTG
2881	TACGGCTACA	. CTAGAAGGAC GATCTTCCTG	AGTATTTGGT TCATAAACCA	ATCTGCGCTC TAGACGCGAG	TGCTGAAGCC	AGTTACCTTC TCAATGGAAG	GGAAAAAGAG	TTGGTAGCTC
2961	TTGATCCGGC AAACAAACC AACTAGGCCG TTTGTTTGG	TTGATCCGGC AAACAAACCA AACTAGGCCG TTTGTTTGGT	CCGCTGGTAG	CGGTGGTTTT	TTTGTTTGCA AAACAAAGGT	AGCAGCAGAT TCGTCGTCTA	TACGCGCAGA	AAAAAAGGAT TTTTTCCTA
3041	CTCAAGAAGA TCCTTTGAT GAGTTCTTCT AGGAAACTA	TCCTTTGATC AGGAACTAG	TTTTCTACGG AAAAGATGCC	GGTCTGACGC CCAGACTGCG	TCAGTGGAAC AGTCACCTTG	GAAAACTCAC CTTTTGAGTG	GTTAAGGGAT	TTTGGTCATG
3121	AGATTATCAA TCTAATAGTT	AAAGGATCTT TTTCCTAGAA	CACCTAGATC GTGGATCTAG	CTTTTAAATT GAAAATTTAA	AAAAATGAAG TTTTACTTC	TTTTAAATCA AAAAATGA AAAATTTAGT	ATCTAAAGTA TAGATTTCAT	TATATGAGTA ATATACTCAT
3201	AACTTGGTCT TTGAACCAGA	AACTIGGICI GACAGTIACC ITGAACCAGA CIGICAAIGG	AATGCTTAAT TTACGAATTA	CAGTGAGGCA GTCACTCCGT	CCTATCTCAG GGATAGAGTC	CGATCTGTCT GCTAGA	ATTTCGTTCA TAAAGCAAGT	TCCATAGTTG AGGTATCAAC
3281	CCTGACTCCC GGACTGAGGG	CGTCGTGTAG GCAGCACATC	ATAACTACGA TATTGATGCT	TACGGGAGGG	CTTACCATCT	GGCCCCAGTG	CTGCAATGAT GACGTTACTA	ACCGCGAGAC TGGCGCTCTG
3361	CCACGCTCAC CGGCTCCAGA GGTGCGAGTG GCCGAGGTCT		TTTATCAGCA AAATAGTCGT	ATAAACCAGC TATTTGGTCG	CAGCCGGAAG	GGCCGAGCGC AGAAGTGGTC CCGGCTCGCG TCTTCACCAG	ľ	CTGCAACTTT
3441	ATCCGCCTCC ATCCAGTCTA TAGGCGGAGG TAGGTCAGAT		TTAATTGTTG AATTAACAAC	CCGGGAAGCT	AGAGTAAGTA (GTTCGCCAGT I	TAATAGTTTG (CGCAACGTTG

FIG. 7-Page 5

2081	CCAGCCATCT	CCAGCCATCT GTTGTTTGCC GGTCGGTAGA CAACAAACGG		GCCTTCCTTG CGGAAGGAAC	pCMV-II CCTCCCCGT GCCTTCCTTG ACCCTGGAAG GGAGGGGGCA CGGAAGGAAC TGGGACCTTC	GTGCCACTCC CACGGTGAGG	GTGCCACTCC CACTGTCCTT TCCTAATAAA CACGGTGAGG GTGACAGGAA AGGATTATTT	TCCTAATAAA AGGATTATTT
2161	ATGAGGAAAT TACTCCTTTA	ATGAGGAAAT TGCATCGCAT TGTCTGAGTA TACTCCTTTA ACGTAGCGTA ACAGACTCAT	TGTCTGAGTA ACAGACTCAT	GGTGTCATTC	TGTCTGAGTA GGTGTCATTC TATTCTGGGG GGTGGGGGTGG GGCAGGACAG CAAGGGGGAG ACAGACTCAT CCACAGTAAG ATAAGACCCC CCACCCCACC	GGTGGGGTGG	GGCAGGACAG	CAAGGGGGAG
2241	GATTGGGAAG CTAACCCTTC	GATTGGGAAG ACAATAGCAG CTAACCCTTC TGTTATCGTC	GATTGGGAAG ACAATAGCAG GCATGCTGGG GAGCTCTTCC GCTTCCTCGC TCACTGACTC GCTGCGCTCG GTCGTTCGGC CTAACCCTTC TGTTATCGTC CGTACGACCC CTCGAGAAGG CGAAGGAGCG AGTGACTGAG CGACGCGAGC CAGCAAGCCG	GAGCTCTTCC CTCGAGAAGG	GCATGCTGGG GAGCTCTTCC GCTTCCTCGC TCACTGACTC GCTGCGCTCG GTCGTTCGGC CGTACGACCC CTCGAGAAGG CGAAGGAGCG AGTGACTGAG CGACGCGAGC CAGCAAGCCG	TCACTGACTC	GCTGCGCTCG	GTCGTTCGGC
2321	TGCGGCGAGC ACGCCGCTCG	TGCGGCGAGC GGTATCAGCT ACGCCGCTCG CCATAGTCGA	CACTCAAAGG CGGTAATACG GTTATCCACA GAATCAGGGG ATAACGCAGG AAAGAACATG GTGAGTTTCC GCCATTAIGC CAATAGGTGT CTTAGTCCCC TATTGCGTCC TTTCTTGTAC	CGGTAATACG GCCATTATGC	CACTCAAAGG CGGTAATACG GTTATCCACA GAATCAGGGG ATAACGCAGG GTGAGTTTCC GCCATTATGC CAATAGGTGT CTTAGTCCCC TATTGCGTCC	GAATCAGGG	ATAACGCAGG TATTGCGTCC	AAAGAACATG TTTCTTGTAC
2401	TGAGCAAAAG ACTCGTTTTC	GCCAGCAAAA CGGTCGTTTT	TGAGCAAAAG GCCAGCAAAA GGCCAGGAAC CGTAAAAAGG CCGCGTTGCT GGCGTTTTTC CATAGGCTCC GCCCCCTGA ACTCGTTTTC CGGTCGTTTT CCGGTCCTTG GCATTTTTCC GGCGCAACGA CCGCAAAAAG GTATCCGAGG CGGGGGGACT	CGTAAAAAGG CCGCGTTGCT GCATTTTTCC GGCGCAACGA	CCGCGTTGCT	GGCGTTTTTC	CATAGGCTCC GTATCCGAGG	GCCCCCTGA
2481	CGAGCATCAC GCTCGTAGTG	AAAAATCGAC TTTTTAGCTG	CGAGCATCAC AAAAATCGAC GCTCAAGTCA GAGGTGGCGA AACCCGACAG GACTATAAAG ATACCAGGCG TTTCCCGCTG GCTCGTAGTG TTTTTAGCTG CGAGTTCAGT CTCCACCGCT TTGGGCTGTC CTGATATTTC TATGGTCCGC AAAGGGGGAC	GAGGTGGCGA	AACCCGACAG TTGGGCTGTC	GACTATAAAG CTGATATTTC	ATACCAGGCG TATGGTCCGC	TTTCCCCCTG
2561	GAAGCTCCCT CGTGCGCTCT CTTCGAGGGA GCACGCGAGA	ŀ	CCTGTTCCGA CCCTGCCGCT TACCGGATAC CTGTCCGCCT TTCTCCCTTC GGGAAGCGTG GAACAAGGCT GGGACGGCGA ATGGCCTATG GACAGGCGGA AAGAGGGAAG CCCTTCGCAC	CCCTGCCGCT	CCCTGCCGCT TACCGGATAC CTGTCCGCCT GGGACGCCGA ATGCCCTATG GACAGGCGGA	CTGTCCGCCT	TTCTCCCTTC AAGAGGGAAG	GGGAAGCGTG

FIG. 7-Page 4

GCGCTTTCTC AATGCTCACG CTGTAGGTAT CTCAGTTCGG TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG TGCACGAACC CGCGAAAGAG TTACGAGTGC GACATCCATA GAGTCAAGCC ACATCCAGCA AGCGAGGTTC GACCCGACAC ACGTGCTTGG

2641

2721

CCCCGTTCAG CCCGACCGCT GCGCCTTATC CGGTAACTAT CGTCTTGAGT CCAACCCGGT AAGACACGAC TTATCGCCAC GGGGCAAGTC GGGCTGGCGA CGCGGAATAG GCCATTGATA GCAGAACTCA GGTTGGGCCA TTCTGTGCTG AATAGCGGTG

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1441	TATTTACAAA ATAAATGTTT	\ TTCACATATA F AAGTGTATAT	CAACAACGCC		pCMV-II GTCCCCGTG CCCGCAGTTT CAGGGGGCAC GGCGTCAAA	TTATTAAACA AATAATTTGT	TAGCGTGGGA ATCGCACCCT	TCTCCGACAT AGAGGCTGTA
1521	CTCGGGTACG GAGCCCATGC	CTCGGGTACG TGTTCCGGAC GAGCCCATGC ACAAGGCCTG	ATGGGCTCTT TACCCGAGAA	CTCCGGTAGC GAGGCCATCG	GGCGGAGCTT	CCACATCCGA GGTGTAGGCT	GCCCTGGTCC	CATCCGTCCA
1601	GCGGCTCATG CGCCGAGTAC	GTCGCTCGCC	AGCTCCTTGC TCGAGGAACG	TCCTAACAGT AGGATTGTCA	GGAGGCCAGA	CTTAGGCACA	GCACAATGCC	CACCACCACC
1681	AGTGTGCCGC TCACACGGCG	AGTGTGCGGC ACAAGGCCGT TCACACGGCG TGTTCCGGCA	GGCGGTAGGG CCGCCATCCC	TATGTGTCTG	AAAATGAGCT TTTTACTCGA	CGGAGATTGG GCCTCTAACC	GCTCGCACCT	GGACGCAGAT
1761	GGAAGACTTA CCTTCTGAAT	GGAAGACTTA AGGCAGCGC CCTTCTGAAT TCCGTCGCCG	AGAAGAAGAT TCTTCTTCTA	GCAGGCAGCT	GAGTTGTTGT CTCAACAACA	ATTCTGATAA TAAGACTATT	GAGTCAAGGG	TAACTCCCGT ATTGAGGGCA
1841	TGCGGTGCTG ACGCCACGAC	TGCGGTGCTG TTAACGGTGG ACGCCACGAC AATTGCCACC	AGGCCAGTGT TCCCGTCACA	AGTCTGAGCA TCAGACTCGT	GTACTCGTTG	CTGCCGCGC CGCCACCAGA GACGCGCGC GCGGTGGTCT		CATAATAGCT GTATTATCGA
1921	GACAGACTAA CTGTCTGATT	CAGACTGTTC GTCTGACAAG	CTTTCCATGG	GTCTTTTCTG	CAGTCACCGT (GTCAGTGCCA)	CGTCGACCTA A	EcoRI AGAATTCAGA TCTTAAGTCT	CTCGAGCAAG
2001	XbaI TCTAGAAAGG AGATCTTTCC	CGCGCCAAGA	BamHI TATCAAGGAT C ATAGTTCCTA G	Mlul CACTACGCG GTGATGCGC	TTAGAGCTCG (CTGATCAGCC TCGACTGTGC GACTAGTCGG AGCTGACACG	1	CTTCTAGTTG

FIG. 7-Page 3

pCMV-II

				<u>م</u>	pCMV-II			
721	GCCTGGCATT CGGACCGTAA	ATGCCCAGTA TACGGGTCAT	CATGACCTTA GTACTGGAAT	CGGGACTTTC GCCCTGAAAG	CTACTTGGCA GATGAACCGT	GTACATCTAC CATGTAGATG	GTATTAGTCA CATAATCAGT	TCGCTATTAC AGCGATAATG
801	CATGGTGATG GTACCACTAC	CGGTTTTGGC GCCAAAACCG	AGTACACCAA TCATGTGGTT	TGGGCGTGGA ACCGGCACCT	TAGCGGTTTG ATCGCCAAAC	ACTCACGGGG TGAGTGCCCC	ATTTCCAAGT TAAAGGTTCA	CTCCACCCCA
881	TTGACGTCAA TGGGAGTTT AACTGCAGTT ACCCTCAAA	TGGGAGTTTG ACCCTCAAAC	TTTTGGCACC AAAACCGTGG	AAAATCAACG TTTTAGTTGC	GGACTTTCCA CCTGAAAGGT	AAATGTCGTA TTTACAGCAT	ATAACCCCGC TATTGGGGCG	CCCGTTGACG GGGCAACTGC
961	CAAATGGGCG GTTTACCCGC	CAAATGGGCG GTAGGCGTGT GTTTACCCGC CATCCGCACA	ACGGTGGGAG TGCCACCCTC	GTCTATATAA CAGATATATT	GCAGAGCTCG	TTTAGTGAAC AAATCACTTG	CGTCAGATCG GCAGTCTAGC	CCTGGAGACG
1041	CCATCCACGC	TGTTTTGACC	TCCATAGAAG AGGTATCTTC	ACACCGGGAC TGTGGCCCTG	CGATCCAGCC GCTAGGTCGG	TCCGCGGCCG	GGAACGGTGC CCTTGCCACG	ATTGGAACGC TAACCTTGCG
1121	GGATTCCCCG CCTAAGGGGC	TGCCAAGAGT ACGGTTCTCA	GACGTAAGTA CTGCATTCAT	CCGCCTATAG	ACTCTATAGG TGAGATATCC	CACACCCCTT	TGGCTCTTAT	GCATGCTATA CGTACGATAT
1201	CTGTTTTGG GACAAAACC	CTTGGGGCCT GAACCCCGGA	ATACACCCCC TATGTGGGGG	GCTCCTTATG	CTATAGGTGA	TGGTATAGCT ACCATATCGA	TAGCCTATAG	GTGTGGGTTA
1281	TTGACCATTA	TTGACCACTC AACTGGTGAG	CCCTATTGGT GGGATAACCA	GACGATACTT CTGCTATGAA	TCCATTACTA AGGTAATGAT	ATCCATAACA TAGGTATTGT	TGGCTCTTTG ACCGAGAAAC	CCACAACTAT
1361	CTCTATTGGC GAGATAACCG	CTCTATTGGC TATATGCCAA GAGATAACCG ATATACGGTT	TACTCTGTCC ATGAGACAGG	TTCAGAGACT	GACACGGACT CTGTGCCTGA	CTGTATTTTT GACATAAAAA	ACAGGATGGG TGTCCTACCC	GTCCATTTAT

FIG. 7-Page 2

H	TCGCGCGTTT AGCGCGCAAA	CGGTGATGAC GCCACTACTG	GGTGAAAACC CCACTTTTGG		pCMV-II TCTGACACAT GCAGCTCCCG AGACTGTGTA CGTCGAGGGC	GAGACGGTCA CTCTGCCAGT	CAGCTTGTCT GTCGAACAGA	GTAAGCGGAT CATTCGCCTA
81	GCCGGGAGCA CGGCCCTCGT	GACAAGCCCG CTGTTCGGGC	TCAGGGGGGG	TCAGCGGGTG	TTGGCGGGTG	TCGGGGCTGG	CTTAACTATG	CGGCATCAGA
161	GCAGATTGTA CGTCTAACAT	CTGAGAGTGC GACTCTCACG	ACCATATGAA TGGTATACTT	GCTTTTTGCA CGAAAAACGT	AAAGCCTAGG TTTCGGATCC	CCTCCAAAAA	AGCCTCCTCA TCGGAGGAGT	CTACTTCTGG
241	AATAGCTCAG TTATCGAGTC	AATAGCTCAG AGGCCGAGGC TTATCGAGTC TCCGGCTCCG	GGCCTCGGCC CCGGAGCCGG	TCTGCATAAA AGACGTATTT	TAAAAAAAT ATTTTTTA	TAGTCAGCCA	TGGGGCGGAG	AATGGGCGGA
321	ACTGGGCGGG TGACCGGCC	GAGGGAATTA CTCCCTTAAT	TTGGCTATTG AACCGATAAC	GCCATTGCAT CGGTAACGTA	ACGTTGTATC TGCAACATAG	TATATCATAA ATATAGTATT	TATGTACATT ATACATGTAA	TATATTGGCT ATATAACCGA
401	CATGTCCAAT GTACAGGTTA	ATGACCGCCA TACTGGCGGT	TGTTGACATT ACAACTGTAA	GATTATTGAC	TAGTTATTAA ATCAATAATT	TAGTAATCAA ATCATTAGTT	TTACGGGGTC	ATTAGTTCAT TAATCAAGTA
481	AGCCCATATA TCGGGTATAT	TGGAGTTCCG ACCTCAAGGC	CGTTACATAA GCAATGTATT	CTTACGGTAA GAATGCCATT	ATGGCCCGCC TACCGGGCGG	TGGCTGACCG	CCCAACGACC	CCCGCCCATT
561	GACGTCAATA ATGACGTATO CTGCAGTTAT TACTGCATAO	ATGACGTATG TACTGCATAC	TTCCCATAGT	AACGCCAATA TTGCGGTTAT	GGGACTTTCC CCCTGAAAGG	ATTGACGTCA	ATGGGTGGAG TACCCACCTC	TATTTACGGT ATAAATGCCA
641	AAACTGCCCA CTTGGCAGTA TTTGACGGGT GAACCGTCAI	CTTGGCAGTA GAACCGTCAT	CATCAAGTGT GTAGTTCACA	ATCATATGCC TAGTATACGG	AAGTCCGCCC TTCAGGCGGG	CCTATTGACG GGATAACTGC	TCAATGACGG 'AGTTACTGCC'	TAAATGGCCC

FIG. 7-Page 1

8241	AGGACAGTAT TCCTGTCATA	TTGGTATCTG AACCATAGAC	CGCTCTGCTG	AAGCCAGT TTCGGTCA	PCM V - del NS35 TA CCTTCGGAAA AT GGAAGCCTTT	S AAGAGTTGGT TTCTCAACCA	AGCTCTTGAT TCGAGAACTA	CCGGCAAACA GGCCGTTTGT
8321	AACCACCGCT TTGGTGGCGA	GGTAGCGGTG CCATCGCCAC	GTTTTTTGT CAAAAAACA	TTGCAAGCAG AACGTTCGTC	CAGATTACGC GTCTAATGCG	GCAGAAAAAA	AGGATCTCAA TCCTAGAGTT	GAAGATCCTT
8401	TGATCTTTTC ACTAGAAAAG	TACGGGGTCT ATGCCCCAGA	GACGCTCAGT CTGCGAGTCA	GGAACGAAAA CCTTGCTTTT	CTCACGTTAA GAGTGCAATT	GGGATTTTGG CCCTAAAACC	TCATGAGATT AGTACTCTAA	ATCAAAAAGG TAGTTTTTCC
8481	ATCTTCACCT TAGAAGTGGA	ATCTTCACCT AGATCCTTTT TAGAAGTGGA TCTAGGAAAA	AAATTAAAAA TTTAATTTTT	TGAAGTTTTA ACTTCAAAAT	AATCAATCTA TTAGTTAGAT	AAGTATATAT TTCATATATA	GAGTAAACTT CTCATTTGAA	GGTCTGACAG
8561	TTACCAATGC AATGGTTACG	TTACCAATGC TTAATCAGTG AATGGTTACG AATTAGTCAC	AGGCACCTAT TCCGTGGATA	CTCAGCGATC	TGTCTATTTC ACAGATAAAG	GTTCATCCAT	AGTTGCCTGA TCAACGGACT	CTCCCGTCG
8641	TGTAGATAAC ACATCTATTG	TGTAGATAAC TACGATACGG ACATCTATTG ATGCTATGCC	GAGGGCTTAC CTCCCGAATG	CATCTGGCCC GTAGACCGGG	CAGTGCTGCA	ATGATACCGC TACTATGGCG	GAGACCCACG	CTCACCGGCT
8721	CCAGATTTAT GGTCTAAATA	CAGCAATAAA GTCGTTATTT	CCAGCCAGCC	GGAAGGGCCG	AGCGCAGAAG TCGCGTCTTC	TGGTCCTGCA A	ACTITAICCG CCTCCAICCA TGAAAIAGGC GGAGGIAGGI	CCTCCATCCA GGAGGTAGGT
8801	GTCTATTAAT CAGATAATTA	TGTTGCCGGG ACAACGGCCC	AAGCTAGAGT TTCGATCTCA	AAGTAGTTCG CCAGTTAATA TTCATCAAGC GGTCAATTAT	I	GTTTGCGCAA (CGTTGTTGCC /	ATTGCTACAG TAACGATGTC
8881	GCATCGTGGT CGTAGCACCA	GTCACGCTCG	TCGTTTGGTA	TGGCTTCATT ACCGAAGTAA	CAGCICCGGI ICCCAACGAI GICGAGGCCA AGGGIIGCIA		CAAGGCGAGT 1 GTTCCGCTCA A	TACATGATCC ATGTACTAGG

FIG. 5-Page 15

7521	CGCATTGTCT GCGTAACAGA	GAGTAGGTGT CTCATCCACA	CATTCTATTC GTAAGATAAG	pCN TGGGGGGTGG ACCCCCACC	pCMV-delNS35 regegegee geregegede acceceace ceaececere	GACAGCAAGG	GGGAGGATTG CCCTCCTAAC	GGAAGACAAT CCTTCTGTTA
7601	AGCAGGCATG TCGTCCGTAC	AGCAGGCATG CTGGGGAGCT TCGTCCGTAC GACCCCTCGA	CTTCCGCTTC	CTCGCTCACT	GACTCGCTGC	GCTCGGTCGT	TCGGCTGCGG	CGAGCGGTAT
7681	CAGCTCACTC	AAAGGCGGTA TTTCCGCCAT	ATACGGTTAT TATGCCAATA	CCACAGAATC	AGGGGATAAC TCCCCTATTG	GCAGGAAAGA CGTCCTTTCT	ACATGTGAGC TGTACACTCG	AAAAGGCCAG TTTTCCGGTC
7761	CAAAAGGCCA GTTTTCCGGT	GGAACCGTAA CCTTGGCATT	AAAGGCCGCG TTTCCGGCGC	TTGCTGGCGT AACGACCGCA	TTTTCCATAG AAAAGGTATC	GCTCCGCCCC	CCTGACGAGC	ATCACAAAAA TAGTGTTTTT
7841	TCGACGCTCA AGCTGCGAGT	AGTCAGAGGT TCAGTCTCCA	GGCGAAACCC CCGCTTTGGG	GACAGGACTA	TAAAGATACC ATTTCTATGG	AGGCGTTTCC TCCGCAAAGG	CCCTGGAAGC	TCCCTCGTGC AGGGAGCACG
7921	GCTCTCCTGT CGAGAGGACA	TCCGACCCTG AGGCTGGGAC	CCGCTTACCG	GATACCTGTC CTATGGACAG	CGCCTTTCTC	CCTTCGGGAA	GCGTGGCGCT	TTCTCAATGC AAGAGTTACG
8001	TCACGCTGTA AGTGCGACAT	GGTATCTCAG CCATAGAGTC	TTCGGTGTAG AAGCCACATC	GTCGTTCGCT	CCAAGCTGGG	CTGTGTGCAC	GAACCCCCCC	TTCAGCCCGA
8081	CCGCTGCGCC	TTATCCGGTA AATAGGCCAT	ACTATCGTCT TGATAGCAGA	TGAGTCCAAC ACTCAGGTTG	CCGGTAAGAC	ACGACTTATC TGCTGAATAG	GCCACTGGCA	GCAGCCACTG
8161	GTAACAGGAT CATTGTCCTA	TAGCAGAGCG ATCGTCTCGC	AGGTATGTAG TCCATACATC	GCGGTGCTAC	AGAGTTCTTG TCTCAAGAAC	AAGTGGTGGC TTCACCACCG	CTAACTACGG	CTACACTAGA

FIG. 5-Page 14

E I N R V A A C L R K L G V P P L R A W R H R GAAATCAATA GGGTGGCGC ATGCCTCAGA AAACTTGGG TACCGCCCTT GCGAGCTTGG AGACACGGG CTTTAGTTAT CCCACCGGCG TACGGAGTCT TTTGAACCCC ATGGCGGGAA CGCTCGAACC TCTGTGGCCC GAGAGGTCCA CTCTCCAGGT щ 6961

A R S V R A R L L A R G G R A I C G K Y L F N W A V CCCGGAGCGT CCGCGCTAGG CTTCTGGCCA GAGGAGGCAG GGCTGCCATA TGTGGCAAGT ACCTCTTCAA CTGGGCAGTA GGGCCTCGCA GGCGCGATCC GAAGACCGGT CTCCTCCGTC CCGACGGTAT ACACCGTTCA TGGAGAAGTT GACCCGTCAT 7041

R T K L K L T P I A A G Q L D L S G W F T A G Y S G AGAACAAAGC TCAAACTCAC TCCAATAGCG GCCGCTGGCC AGCTGGACTT GTCCGGCTGG TTCACGGCTG GCTACAGCGG TCTTGTTTCG AGTTGAGTG AGGTTATCGC CGGCGACCGG TCGACCTGAA CAGGCCGACC AAGTGCCGAC CGATGTCGCC 7121

G D I Y H S V S H A R P R W I W F C L L L L A A G V GGGAGACATT TATCACAGGG TGTCTCATGC CCGGCCCGG TGGATCTGGT TTTGCCTACT CCTGCTTGCT GCAGGGGTAG CCTCTGTAA ATAGTGTCGC ACAGAGTACG GGCCGGGGGCG ACCTAGACCA AAACGGATGA GGACGAACGA CGTCCCCATC +7

BamHI MluI

GTAGACAACA GCTCGCTGAT CAGCCTCGAC TGTGCCTTCT AGTTGCCAGC CATCTGTTGT TCAACGGICG ACACGGAAGA GTCGGAGCTG CGAGCGACTA AGGATCCACT ACGCGTTAGA TGCGCAATCT TCCTAGGTGA CAAGATATCA GTTCTATAGT 7361

GAAATTGCAT GGAAGGTGCC ACTCCCACTG TCCTTTCCTA ATAAAATGAG CCTTCCACGG TGAGGGTGAC AGGAAAGGAT TATTTTACTC GGGCACGGAA GGAACTGGGA CCTTGACCCT CCCGTGCCTT TTGCCCCTCC AACGGGGAGG 7441

- A A C R A A G L Q D C T M L V C G GCAGCCTGTC GAGCCGCAGG GCTCCAGGAC TGCACCATGC TCGTGTGGG CGTCGGACAG CTCGGCGTCC CGAGGTCCTG ACGTGGTACG AGCACACACC N T L T C Y I K A R AACACCCTCA CTTGCTACAT CAAGGCCCGG TIGIGGAGT GAACGAIGIA GIICCGGGCC +2 6401
- D D L V V I C E S A G V Q E D A A S L R A F T E A M CGACGACTTA GTCGTTATCT GTGAAAGCGC GGGGGTCCAG GAGGACGCG CGAGCCTGAG AGCCTTCACG GAGGCTATGA GCTGCTGAAT CAGCAATAGA CACTTTCGCG CCCCCAGGTC CTCCTGCGCC GCTCGGACTC TCGGAAGTGC CTCCGATACT 6481
- T R Y S A P P G D P Q P E Y D L E L I T S C S S N V CCAGGIACTC CGCCCCCCT GGGACCCC CACAACCAGA ATACGACTTG GAGCTCATAA CATCATGCTC CTCCAACGTG GGTCCATGAG GCGGGGGGG CCCTGGGGG GTGTTGGTCT TATGCTGAAC CTCGAGTATT GTAGTACGAG GAGGTTGCAC
- S V A H D G A G K R V Y Y L T R D P T T P L A R A W W TCAGTCGCC ACGACGCC TGGAAAGAG GTCTACTACC TCACCCGTGA CCCTACAACC CCCCTCGCGA GAGCTGCGTG AGTCAGCGGG TGCTGCCGC ACGTTTCTCC CAGATGATGG AGTGGGCACT GGGATGTTGG GGGAGCGCT CTCGACGCAC +5 6641
- AGACACACTC CAGTCAATTC CTGGCTAGGC AACATAATCA TGTTTGCCCC CACACTGTGG GCGAGGATGA TCTGTGTGG GTCAGTTAAG GACCGATCCG TTGTATTAGT ACAAACGGGG GTGTGACACC CGCTCCTACT T L W F A P GGAGACAGCA AGACACACTC CAGTCAATTC CTGGCTAGGC G I M S z > CCTCTGTCGT 6721
- +2 I L M T H F F S V L I A R D Q L E Q A L D C E I Y G A ATGUERICATION CONTINUES OF TACGGGGCC CCATTION AGGINATION AGGINATION ATGUERA CAGGINA CAGGINA ATGANAN AGGINA ATGANAN AT 6801
- C Y S I E P L D L P P I I Q R L H G L S A F S L H S Y TGCTACTCCA TAGAACCACT GGATCTACCT CCAATCATTC AAAGACTCCA TGGCCTCAGC GCATTTTCAC TCCACAGTTA ACGATGAGGT ATCTTGGTGA CCTAGATGGA GGTTAGTAAG TTTCTGAGGT ACCGGAGTCG CGTAAAAGTG AGGTGTCAAT

V L V L N P S V A A T L G F G A Y M S K GTGCTAGTAC TCAACCCCTC TGTTGCTGCA ACACTGGGCT TTGGTGCTTA CATGTCCAAG CACGATCATG AGTTGGGGAG ACAACGACGT TGTGACCCGGA AACCACGAAT GTACAGGTTC Y A A Q G Y K ATGCAGCTCA GGCTATAAG TACGTCGAGT CCCGATATTC

A H G I D P N I R T G V R T I T G S P I T Y S T Y G GCTCATGGGA TCGATCCTAA CATCAGGAA CAATTACCAC TGGCAGCCC ATCACGTACT CCACCTACGG CGAGTACCT AGCTAGGATT GTAGTCCTGG CCCCACTCTT GTTAATGGTG ACCGTCGGGG TAGTGCATGA GGTGGATGCC +5 2081

K F L A D G G C S G G A Y D I I C D E C H S T D A CAAGTICCTI GCCGACGCG GGTGCTCGG GGGCGCTTAI GACATAATAA TITGTGACGA GTGCCACTCC ACGGATGCCA GTTCAAGGAA CGCCTGCCGC CCACGAGCCC CCCGCGGAATA CTGTATTATT AAACACTGCT CACGGTGAGG TGCCTACGGT 2161

T S I L G I G T V L D Q A E T A G A R L V V L A T A T A CATCCATCTT GGGCATTGGC ACTGTCCTTG ACCAAGCAGA GACTGCGGG GCGAGACTGG TTGTGCTCGC CACCGCCACCGTAGGAAC TGGTTCGTCT CTGACGCCCC CGCTCTGACC AACACGAGCG GTGGCGGTGG 2241

P P G S V T V P H P N I E E V A L S T T G E I P F Y G CCTCCGGGGCT CCGTCACTGT GCCCCATCC AACATCGAGG AGGTTGCTCT GTCCACCACC GGAGAGATCC CTTTTTACGG GGAGGCCCGA GGCAGTGACA CGGGGTAGGG TTGTAGCTCC TCCAACGAGA CAGGTGGTGG CCTCTCTAGG GAAAAATGCC +2 2321

K A I P L E V I K G G R H L I F C H S K K C D E L CAAGGCTATC CCCCTCGAAG TAATCAAGG GGGGAGACAT CTCATCTTCT GTCATTCAAA GAAGAAGTGC GACGAACTCG GTTCCGATAG GGGGAGCTTC ATTAGTTCCC CCCCTCTGTA GAGTAGAAG CAGTAAGTTT CTTCTTCACG CTGCTTGAGC 2401

A A K L V A L G I N A V A Y Y R G L D V S V I P T S G CCGCAAAGCT GGTCGCATTG GGCATCAATG CCGTGGCCTA CTACCGCGGT CTTGACGTGT CCGTCATCCC GACCAGCGGC GGCGTTTCGA CCAGCGTAAC CCGTAGTTAC GGCACCGGAT GATGGCGCGCA GAACTGCACA GGCAGTAGGG CTGGTCGCCG +5 2481

V R C H A R K A V T H I N S V W K D L L E D N CGTCCGTTGC CATGCCAGAA AGGCCGTAAC CCACATCAAC TCCGTGTGGA AAGACCTTCT GGAAGACAAT GCAGGCAACG GTACGGTCTT TCCGGCATTG GGTGTAGTTG AGGCACACCT TTCTGGAAGA CCTTCTGTTA CCCGTTTTCT GCAGGCAACG GGGCAAAAGA ď 5841

AAGGGGGTC GTAAGCCAGC TTCCCCCCAG CATTCGGTCG G ტ V T P I D T T I M A K N E V F C V Q P E GTAACACCAA TAGACACTAC CATCATGGCT AAGAACGAGG TTTTCTGCGT TCAGCCTGAG CATTGTGGTT ATCTGTGATG GTAGTACCGA TTCTTGCTCC AAAAGACGCA AGTCGGACTC +5 5921

V F P D L G V R V C E K M A L Y D V V T K L P GTGTTCCCCG ATCTGGGCGT GCGCGTGTGC GAAAGATGG CTTTGTACGA CGTGGTTACA AAGCTCCCCT CACAAGGGC TAGACCGCA CGCGCACACG CTTTTCTACC GAAACATGCT GCACCAATGT TTCGAGGGA R L I TCGTCTCATC AGCAGAGTAG 6001

× 3 A 0 E F EcoRI 0 Ç \succ 0 بعآ G Ы S S G Σ ¥ Н +2

S

GTTGAATTCC TCGTGCAAGC GTGGAAGTCC CAACTTAAGG AGCACGTTCG CACCTTCAGG AGGACAGCGG TCCTGTCGCC GGGAAGCTCC TACGGATTCC AATACTCACC CCCTTCGAGG ATGCCTAAGG TTATGAGTGG TGGCCGTGAT ACCGGCACTA 6081

K K T P M G F S Y D T R C F D S T V T E S D I R T E E AAGAAAACC CAATGGGGTT CTCGTATGAT ACCCGCTGCT TTGACTCCAC AGTCACTGAG AGCGACATCC GTACGGAGGA TTCTTTTGGG GTTACCCCAA GAGCATACTA TGGGCGACGA AACTGAGGTG TCAGTGACTC TCGCTGTAGG CATGCCTCT 6161

GTGGCCATCA AGTCCCTCAC CGAGGGCTT TATGTTGGGG CACCGGTAGT TCAGGGAGTG GCTCTCCGAA ATACAACCCC 戸 Ц တ V A I A I Y Q C C D L D P Q A R GGCAATCTAC CAATGTTGTG ACCTCGACCC CCAAGCCCGC CCGTTAGATG GTTACAACAC TGGAGCTGGG GGTTCGGGCG 6241

GENCGRATOR RCRASCO GOORGE A L L L L L CONTROL GCCCTCTTAC CAATTCAAGG CGGGAGAATG GTTAAGTTCC S

S T L S T A L A E L A T R S F G S S T S G I T G D ATCAACCCTA TCTACTGCCT TGGCGAGCT CGCCACCAGA AGCTTTGGCA GCTCCTCAAC TTCCGGCATT ACGGCGCACA TAGTTGGGAT AGATGACGA ACCGGCTCGA GCGGTGGTCT TCGAAACCGT CGAGGAGTTG AAGGCCGTAA TGCCCGCTGT

N T T T S S E P A P S G C P P D S D A E S Y S S M P P ATACGACAAC ATCCTCTGAG CCCGCCCCTT CTGCTGCCC CCCGACTCC GACGCTGAGT CCTATTCCTC CATGCCCCCC TATGCTGTTG TAGGAGACTC GGGCGGGGAA GACCGACGGG GGGCTGAGG CTGCGACTCA GGATAAGGAG GTACGGGGGG

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+2

GAGGCCAACG CGGAGGAIGT CTCCGGTTGC GCCTCCTACA CATGGTCAAC GGTCAGTAGT GACCICCCC TCGGACCCCT AGGCCTAGAA TCGCTGCCCA GTACCAGTIG CCAGICATCA CIGGAGGGG AGCCIGGGA ICCGGAICIT AGCGACGGGI 5441

V C C S M S Y S W T G A L V T P C A A E E Q K L P I CGTGTGCTGC TCAATGTCTT ACTCTTGGAC AGGCGCACTC GTCACCCCGT GCGCCGCGGA AGAACAGAAA CTGCCCATCA GCACACGACG AGTTACAGAA TGAGAACCTG TCCGCGTGAG CAGTGGGGCA CGCGGCGCCT TCTTGTCTTT GACGGGTAGT 5521

N A L S N S L L R H H N L V Y S T T S R S A C Q R Q K ATGCACTAAG CAACTCGTTG CTACGTCACC ACAATTTGGT GTATTCCACC ACCTCACGCA GTGCTTGCCA AAGGCAGAAG TACGTGATTC GTTGAGCAAC GATGCAGTGG TGTTAAACCA CATAAGGTGG TGGAGTGCGT CACGAACGGT TTCCGTCTTC +5

AAAGTCACAT TTGACAGACT GCÀAGTTCTG GACAGCCATT ACCÀGGACGT ACTCAAGGAG GTTAAAGCAG CGGCGTCAAA TTTCAGTGTA AACTGTCTGA CGTTCAAGAC CTGTCGGTAA TGGTCCTGCA TGAGTTCCTC CAATTTCGTC GCCGCAGTTT L O O H Д O V R Ω 5681

V K A N L L S V E E A C S L T P P H S A K S K F G Y AGTGAAGGCT AACTTGCTAT CCGTAGAGGA AGCTTGCAGC CTGACGCCCC CACACTCAGC CAAATCCAAG TTTGGTTATG TCACTTCCGA TTGAACGATA GGCATCTCCT TCGAACGTCG GACTGCGGG GTGTGAGTCG GTTTAGGTTC AAACCAATAC 5761

P C E P E P D V A V L T S M L T D CCTTGCGAGC CCGAACCGGA CGTGGCCGTG TTGACGTCCA TGCTCACTGAGGACGCTCG GCGTGGCCTC GCACCGCCAC AACTGCAGGT ACGAGTGACT L H E Y P V G S Q L CTCCACGAAT ACCCGGTAGG GTCGCAATTA GAGGTGCTTA TGGGCCATCC CAGCGTTAAT

4801

L K A T C T A N H D S P D A E L I E A N CTCAAGGCAA CTTGCACGC TAACCATGAC TCCCCTGATG CTGAGCTCAT AGAGGCCAAC CGGTCGATAG GCGAGGTAGA GAGTTCCGTT GAACGTGGCG ATTGGTACTG AGGGGACTAC GACTCGAGTA TCTCCGGTTG S Q L S A P S GCCAGCTATC CGCTCCATCT 4881

L L W R Q E M G G N I T R V E S E N K V V I L D S F D CTCCTATGGA GGCAGGAGAT GGGCGGCAAC ATCACCAGGG TTGAGTCAGA AAACAAAGTG GTGATTCTGG ACTCCTTCGA GAGGATACCT CCGTCCTCTA CCGGCCGTTG TAGTGGTCCC AACTCAGTCT TTTGTTTCAC CACTAAGACC TGAGGAAGCT

P L V A E E D E R E I S V P A E I L R K S R R F A ·Q TCCGCTTGTG GCGGAGGAGG ACGAGCGGGA GATCTCCGTA CCCGCAGAAA TCCTGCGGAAA GTCTCGGAGA TTCGCCCAGG AGGCGAACAC CGCCTCCTCC TGCTCGCCCT CTAGAGGCAT GGGCGTCTTT AGGACGCCTT CAGAGCCTCT AAGCGGGTCC 5041

CCTGCCCGT TTGGGCGCGG CCGGACTATA ACCCCCCGCT AGTGGAGAGG TGGAAAAAGC CCGACTACGA ACCACCTGTG GGGACGGGCA AACCCGCGCC GGCCTGATAT TGGGGGGCGA TCACCTCTGC ACCTTTTTCG GGCTGATGCT TGGTGGACAC 团 Ъ P D Y N W A R 5121

CGGACGGTGG TCCTCACTGA GCCTGCCACC AGGAGTGACT T 2 V H G C P L P P K S P V P P P K K GICCATGGCT GCCGCTTCC ACCTCCAAGA TCCCCTCCTG TGCCTCCGC TCGGAAGAAG CAGGTACCGA CGGGGGAGGG AGCCTTCTTC

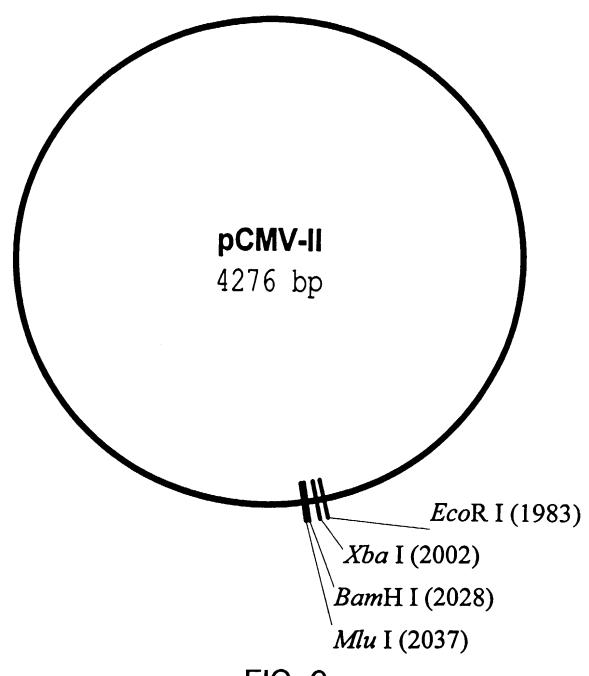


FIG. 6

8961	CCCATGTTGT GGGTACAACA	GCAAAAAGC	GGTTAGCTCC CCAATCGAGG	TTCGGTC	pCMV-delNS35 TTCGGTCCTC CGATCGTTGT AAGCCAGGAG GCTAGCAACA	CAGAAGTAAG GTCTTCATTC	TTGGCCGCAG	TGTTATCACT ACAATAGTGA
9041	CATGGTTATG GTACCAATAC		GCAGCACTGC ATAATTCTCT TACTGTCATG CGTCGTGACG TATTAAGAGA ATGACAGTAC	TACTGTCATG ATGACAGTAC	CCATCCGTAA GGTAGGCATT	GATGCTTTTC CTACGAAAAG	TGTGACTGGT ACACTGACCA	GAGTACTCAA
9121	CCAAGTCATT GGTTCAGTAA	CTGAGAATAG GACTCTTATC	TGTATGCGGC ACATACGCCG	GACCGAGTTG CTGGCTCAAC	CTCTTGCCCG	GCGTCAATAC	GGGATAATAC	CGCGCCACAT
9201	AGCAGAACTT TCGTCTTGAA	TAAAAGTGCT ATTTTCACGA	CATCATTGGA GTAGTAACCT	AAACGTTCTT TTTGCAAGAA	1	CGGGCGAAA ACTCTCAAGG GCCCGCTTT TGAGAGTTCC	ATCTTACCGC TAGAATGGCG	TGTTGAGATC ACAACTCTAG
9281	CAGTTCGATG GTCAAGCTAC	TAACCCACTC ATTGGGTGAG	GTGCACCCAA CACGTGGGTT	CTGATCTTCA	GCATCTTTTA CGTAGAAAAT	CTTTCACCAG	CGTTTCTGGG	TGAGCAAAAA ACTCGTTTTT
9361	CAGGAAGGCA GTCCTTCCGT	CAGGAAGGCA AAATGCCGCA GTCCTTCCGT TTTACGGCGT	AAAAAGGGAA TTTTTCCCTT	TAAGGGCGAC ATTCCCGCTG	ACGGAAATGT TGCCTTTACA		TACTCTTCCT ATGAGAAGGA	TTTTCAATAT
9441	TATTGAAGCA ATAACTTCGT	TTTATCAGGG AAATAGTCCC	TTATTGTCTC AATAACAGAG	ATGAGCGGAT TACTCGCCTA	ACATATTTGA TGTATAAACT	ATGTATTTAG AAAAATAAAC AAATAGGGGT TACATAAATC TTTTTATTTG TTTATCCCCA	AAAAATAAAC TTTTTATTTG	AAATAGGGT TTTATCCCCA
9521	TCCGCGCACA	TTTCCCCGAA AAAGGGGCTT	AAGTGCCACC TTCACGGTGG	TGACGTCTAA ACTGCAGATT	GAAACCATTA CTTTGGTAAT	TTATCATGAC ATTAACCTAT AATAGTACTG TAATTGGATA		AAAATAGGC TTTTTATCCG
9601	GTATCACGAG GCCCTTTCGT CATAGTGCTC CGGGAAAGCA		5					

FIG. 5-Page 16

- P C S G S W L R D I W D W I C E V L S D CATGCTCCG GTTCCTGGCT AAGGGACATC TGGGACTGGA TATGCGAGGT GTTGAGCGAC GGTACGAGGC CAAGGACGGA TTCCCTGTAG ACCCTGACCT ATACGCTCCA CAACTCGCTG TAAGCTCGGA GTGTACCACT ATTCGAGCCT CACATGGTGA တ 4161
- S \succ G 24 0 C S > BamHI Ġ Н 0 Д Σ Н \bowtie A П 3 \vdash × Ŀ +2
- CTTTGTGTCC TGCCAGCGCG GGTATAAGGG CCATATTCCC ACGGTCGCGC GGTGTCGACG GACCCTAGGG GAAACACAGG CTGGGATCCC CCACAGCTGC TAAGCTCATG AAATTCTGGA CCGATTTTCG ATTCGAGTAC GGCTAAAAGC TTTAAGACCT 4241
- AACGGGACGA TIGCCCIGCT G V W R G D G I M H T R C H C G A E I T G H V K GGTCTGGCGA GGGGACGCA TCATGCACAC TCGCTGCCAC TGTGGAGCTG AGATCACTGG ACATGTCAAA CCAGACCGCT CCCCTGCCGT AGTACGTGTG AGCGACGGTG ACACCTCGAC TCTAGTGACC TGTACAGTTT 4321
- M R I V G P R T C R N M W S G T F P I N A Y T T G P C TCAGGATCGT CGGTCCTAGG ACCTGCAGGA ACATGTGGAG TGGGACCTTC CCCATTAATG CCTACACCAC GGGCCCTGT ACTCCTAGCA GCCAGGATCC TGGACGTCCT TGTACACCTC ACCCTGGAAG GGGTAATTAC GGATGTGGTG CCCGGGGACA +2 M R 4401
- T P L P A P N Y T F A L W R V S A E E Y V E I R Q V G ACCCCCTTC CTGCGCCGAA CTACACGTTC GCGCTATGGA GGGTGTCTGC AGAGGAATAC GTGGAGATAA GGCAGGTGGG TGGGGGAAG GACGCGGCTT GATGTGCAAG CGCGATACCT CCCACAGACG TCTCCTTATG CACCTCTATT CCGTCCACCC 4481
- K C P C Q V P S P E F F T AAATGCCCGT GCCAGGTCCC ATGCCCGAA TTTTTCACAG TTTACGGGCA CGGTCCAGGG TAGCGGGCTT AAAAAGTGTC D F H Y V T G M T T D N L GGACTTCCAC TACGTGACG GTATGACTAC TGACAATCTT CCTGAAGGTG ATGCACTGCC CATACTGATG ACTGTTAGAA
- H R F A P C K P L L R E E V S F R V G CATAGGTITG CGCCCCCTG CAAGCCCTTG CTGCGGGAGG AGGTATCATT CAGAGTAGGA GTATCCAAAC GCGGGGGGGC GTTCGGGAAC GACGCCCTCC TCCATAGTAA GTCTCATCCT GACGCCTCC TCCATAGTAA GTCTCATCCT E L D G V K L AATTGGACGG GGTGCGCGTA C/ 4641

	ACAGGATGGG
	ATTGGC TATATGCCAA TACTCTGTCC TTCAGAGACT GACAGGACT CTGTATTTT ACAGGATGGG
pCMV-delNS35	GACACGGACT
pCM	TTCAGAGACT
	TACTCTGTCC
	TATATGCCAA
	TTGGC

1361		CTCTATTGGC TATATGCCAA GAGATAACCG ATATACGGTT	TACTCTGTCC ATGAGACAGG	TTCAGA	PCM V-GEINS3S GACT GACAGGGACT CTGA CTGTGCCTGA	CTGTATTTT GACATAAAAA	ACAGGATGGG GTCCATTTAT TGTCCTACCC CAGGTAAATA	GTCCATTTAT CAGGTAAATA
1441		TATTTACAAA TTCACATATA ATAAATGTTT AAGTGTATAT	CAACAACGCC GTTGTTGCGG	GTCCCCCGTG	GTCCCCCGTG CCCGCAGTTT TTATTAAACA CAGGGGCCAC GGCCGTCAAA AATAATTTGT	TTATTAAACA AATAATTTGT	TTATTAAACA TAGCGTGGGA TCTCCGACAT AATAATTTGT ATCGCACCCT AGAGGCTGTA	TCTCCGACAT AGAGGCTGTA
1521		CTCGGGTACG TGTTCCGGAC GAGCCCATGC ACAAGGCCTG	ATGGGCTCTT TACCCGAGAA	CTCCGGTAGC	CTCCGGTAGC GGCGCAGCTT CCACATCCGA GCCCTGGTCC GAGGCCATCG CCGCCTCGAA GGTGTAGGCT CGGGACCAGG	CCACATCCGA		CATCCGTCCA
1601	GCGGCTCATG GTCGCTCG CGCCGAGTAC CAGCGAGC	35	AGCTCCTTGC TCCTAACAGT TCGAGGAACG AGGATTGTCA		GGAGGCCAGA CTTAGGCACA GCACAATGCC CCTCCGGTCT GAATCCGTGT CGTGTTACGG	CTTAGGCACA		CACCACCACC
1681	AGTGTGCCGC TCACACGGCG	AGTGTGCCGC ACAAGGCCGT TCACACGGCG TGTTCCGGCA	GGCGGTAGGG	TATGTGTCTG AAAATGAGGT ATACACAGAC TTTTACTGGA	ľ	CGGAGATTGG GCTCGCACCT GCCTCTAACC CGAGCGTGGA		GGACGCAGAT
1761	GGAAGACTTA CCTTCTGAAT	GGAAGACTTA AGGCAGCGGC CCTTCTGAAT TCCGTCGCCG	AGAAGAAGAT GCAGGCAGCT TCTTCTTCTA CGTCCGTCGA	GCAGGCAGCT	GAGTTGTTGT ATTCTGATAA GAGTCAGAGG CTCAACAACA TAAGACTATT CTCAGTCTCC	ATTCTGATAA TAAGACTATT	GAGTCAGAGG CTCAGTCTCC	TAACTCCCGT
1841	TGCGGTGCTG TTAACGGTGG ACGCCACGAC AATTGCCACC	TTAACGGTGG	AGGGCAGTGT AGTCTGAGCA TCCCGTCACA TCAGACTCGT	AGTCTGAGCA TCAGACTCGT	GTACTCGTTG	CTGCCGCGCG	CGCCACCAGA (CATAATAGCT
+2								M A A
1921	GACAGACTAA CAGACTGTTC						EcoRI	

FIG. 5-Page 3

GACAGACTAA CAGACTGTTC CTTTCCATGG GTCTTTTCTG CAGTCACCGT CGTCGACCTA AGAATTCACC ATGGCTGCAT CTGTCTGATT GTCTGACAAG GAAAGGTACC CAGAAAAGAC GTCAGTGGCA GCAGCTGGAT TCTTAAGTGG TACCGACGTA

641	AAACTGCCCA TTTGACGGGT	CTTGGCAGTA GAACCGTCAT	CATCAAGTGT GTAGTTCACA	ATCATA TAGTA1	PCM V-delNS35 NTGCC AAGTCCGCCC ACGC TTCAGGCGGG	CCTATTGACG GGATAACTGC	TCAATGACGG AGTTACTGCC	TAAATGGCCC ATTTACCGGG
721	GCCTGGCATT CGGACCGTAA	ATGCCCAGTA TACGGGTCAT	CATGACCTTA GTACTGGAAT	CGGGACTTTC	CTACTTGGCA GATGAACCGT	GTACATCTAC	GTATTAGTCA	TCGCTATTAC
801	CATGGTGATG	CGGTTTTGGC GCCAAAACCG	AGTACACCAA TCATGTGGTT	TGGGCGTGGA ACCCGCACCT	TAGCGGTTTG	ACTCACGGGG TGAGTGCCCC	ATTTCCAAGT TAAAGGTTCA	CTCCACCCCA
881	TTGACGTCAA AACTGCAGTT	TGGGAGTTTG ACCCTCAAAC	TTTTGGCACC AAAACCGTGG	AAAATCAACG TTTTAGTTGC	GGACTTTCCA CCTGAAAGGT	AAATGTCGTA TTTACAGCAT	ATAACCCCGC TATTGGGGCG	CCCGTTGACG
961	CAAATGGGCG GTTTACCCGC	CAAATGGGCG GTAGGCGTGT GTTTACCCGC CATCCGCACA	ACGGTGGGAG TGCCACCCTC	GTCTATATAA CAGATATATT	GCAGAGCTCG CGTCTCGAGC	TTTAGTGAAC AAATCACTTG	CGTCAGATCG GCAGTCTAGC	CCTGGAGACG
1041	CCATCCACGC TGTTTTGAC GGTAGGTGCG ACAAAACTG	TGTTTTGACC ACAAAACTGG	TCCATAGAAG AGGTATCTTC	ACACCGGGAC TGTGGCCCTG	CGATCCAGCC	TCCGCGGCCG	GGAACGGTGC	ATTGGAACGC TAACCTTGCG
1121	GGATTCCCCG CCTAAGGGGC	GGATTCCCCG TGCCAAGAGT CCTAAGGGGC ACGGTTCTCA	GACGTAAGTA CTGCATTCAT	CCGCCTATAG	ACTCTATAGG TGAGATATCC	CACACCCCTT TGGCTCTTAT GTGTGGGGAA ACCGAGAATA	ł	GCATGCTATA
1201	CTGTTTTGG CTTGGGGCCT GACAAAACC GAACCCCGGA		ATACACCCCC TATGTGGGGG	GCTCCTTATG	CTATAGGTGA GATATCCACT	TGGTATAGCT TAGCCTATAG ACCATATCGA ATCGGATATC	i	GTGTGGGTTA
1281	TTGACCATTA AACTGGTAAT	TTGACCACTC	CCCTATTGGT	GACGATACTT CTGCTATGAA	TCCATTACTA A	ATCCATAACA TGGCTCTTTG TAGGTATTGT ACCGAGAAAC	1	CCACAACTAT GGTGTTGATA

FIG. 5-Page 2

- L P G N P A I A S L M A F T A A V T S P L T T CTGCTGGTA ACCCCGCCAT TGCTTCATTG ATGCTTTTA CAGCTGCTGT CACCAGCCCA CTAACCACTA GACGCACCAT TGGGGGGTAACCTACCGAAAAT GTCGACGACA GTGGTCGGGT GATTGGTGAT CTTGTCAACG GAACAGTTGC 7 3601
- S Q T L L F N I L G G W V A A Q L A P G A A T A F V GCCAAACCT CCTCTTCAAC ATATTGGGG GGTGGGTGGC TGCCCAGCTC GCCGCCCCG GTGCCGTAC TGCCTTTGTG CGGTTTGGGA GGAGAAGTTG TATAACCCCC CCACCCACCG ACGGGTCGAG CGGCGGGGC CACGGCGATG ACGGAAACAC +5 3681
- G A G L A G A A I G S V G L G K V L I D I L A G Y G A GECGTGGCT TAGTGGCG CGCCATCGGC AGTGTTGGAC TGGGGAAGGT CCTCATAGAC ATCCTTGCAG GGTATGGCGC CGCGACCGC GCGCACCGC ACCCTTCCA GGAGTATCTG TAGGAACGTC CCATACCGCG 3761
- G V A G A L V A F K I M S G E V P S T E D L V N L L GGGCGTGGCG GGAGCTCTTG TGGCATTCAA GATCATGAGC GGTGAGGTCC CCTCCACGGA GGACCTGGTC AATCTACTGC CCCGCACCGC CCTCGAGAAC ACCGTAAGTT CTAGTACTCG CCACTCCAGG GGAGGTGCCT CCTGGACCAG TTAGATGACG
- P A I L S P G A L V V G V V C A A I L R R H V G P G E CCGCCATCCT CTCGCCCGGA GCCCTCGTAG TCGCGTGGT CTGTGCAGCA ATACTGCGCC GGCACGTTGG CCGGGGGAG GGCGGTAGGA GAGCGGGCCT CGGGAGCATC AGCCGCACCA GACACGTCGT TATGACGCGG CCGTGCAACC GGGCCCGCTC 3921
- G A V Q W M N R L I A F A S R G N H V S P T H Y V P E GGGGCAGTGC AGTGGATGAA CCGGCTGATA GCCTTCGCCT CCCGGGGGAA CCATGTTTCC CCCACGCACT ACGTGCCGGA CCCCGTCACG TCACCTACTT GGCGCTAT CGGAAGCGGA GGGCCCCTT GGTACAAAGG GGGTGCGTGA TGCACGGCCT +2 4001
- A A R V T A I L S S L T V T Q L L R R L H Q W GCTGCCCGCG TCACTGCAT ACTCAGCAGC CTCACTGTAA CCCAGCTCCT GAGGCGACTG CACCAGTGGA CGACGGGCGC AGTGACGGTA TGAGTCGTCG GAGTGACATT GGGTCGAGGA CTCCGCTGAC GTGGTCACCT GAGCGATGCA CTCGCTACGT ¥ Д

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1	TCGCGCGTTT AGCGCGCAAA	CGGTGATGACACACACACACACACACACACACACACACAC	GGTGAAAACC	TCTGA	PCM V - GEINSSS SACAT GCAGCTCCCG STGTA CGTCGAGGCC	GAGACGGTCA CTCTGCCAGT	CAGCTTGTCT	GTAAGCGGAT CATTCGCCTA
81	GCCGGGAGCA	GACAAGCCCG		TCAGGGGGG TCAGGGGGTG AGTCGCGGGG AGTCGCCCAC	TTGGCGGGTG	TCGGGGCTGG	CTTAACTATG GAATTGATG	CGCCATCAGA
161	GCAGATTGTA	. CTGAGAGTGC GACTCTCACG	ACCATATGAA TGGTATACTT	GCTTTTTGCA CGAAAAACGT	Stul AAAGCCTAGG CCTCCAAAAA TTTCGGATCC GGAGGTTTTT		AGCCTCCTCA (CTACTTCTGG
241	AATAGCTCAG TTATCGAGTC	AATAGCTCAG AGGCCGAGGC TTATCGAGTC TCCGGCTCCG	GGCCTCGGCC	TCTGCATAAA AGACGTATTT	TAAAAAAAT ATTTTTTA	TAGTCAGCCA	TGGGGGGGGG A	ATTGGGCGGA TTACCCGCCT
321	ACTGGGCGGG TGACCCGCCC	ACTGGGGGG GAGGGAATTA TGACCGCCC CTCCCTTAAT	TTGGCTATTG AACCGATAAC	GCCATTGCAT		TATATCATAA ATATAGTATT	TATGTACATT I	TATATTGGCT ATATAACCGA
401	CATGTCCAAT GTACAGGTTA	CATGTCCAAT ATGACCGCCA GTACAGGTTA TACTGGCGGT	TGTTGACATT ACAACTGTAA	GATTATTGAC CTAATAACTG	TAGTTATTAA TAGTAATCAA ATCAATAATT ATCATTAGTT	I .	TTACGGGGTC ATTAGTTCAT AATGCCCCAG TAATCAAGTA	ATTAGTTCAT TAATCAAGTA
481	AGCCCATATA TCGGGTATAT	TGGAGTTCCG ACCTCAAGGC	CGTTACATAA GCAATGTATT	CTTACGGTAA	ATGGCCCGCC TACCGGGCGG	TGGCTGACCG (ACCGACTGGC)	TGGCTGACG CCCAACGACC CCCGCCCATT ACCGACTGGC GGGTTGCTGG GGGCGGGTAA	CCCGCCCATT
561	GACGTCAATA CTGCAGTTAT	GACGTCAATA ATGACGTATG CTGCAGTTAT TACTGCATAC	TTCCCATAGT	AACGCCAATA TTGCGGTTAT	GGGACTITCC ATTGACGTCA CCCTGAAAGG TAACTGCAGT	ATTGACGTCA FIAACTGCAGT 1	AACGCCAATA GGGACTTTCC ATTGACGTCA ATGGGTGGAG TATTTACGGT TTGCGGTTAT CCCTGAAAGG TAACTGCAGT TACCCACCTC ATAAATGCCA	TATTTACGGT ATAAATGCCA

FIG. 5-Page 1

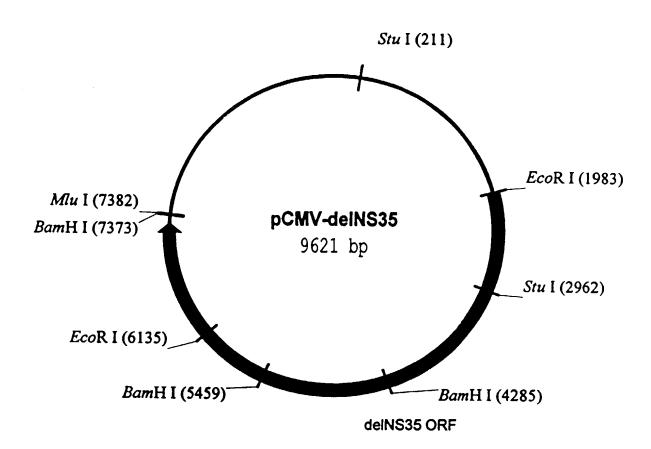


FIG. 4

A T V C A R A Q A P P P S W D Q M W K C L I R L K P T GCCACCACACTGT GCGACCACAC TCAAGCCCAC TCAAGCCCAC GCGTGT GCGAAGTGT TTGATTCGCC TCAAGCCCAC CGGTGGCACAC GCGGATCCCG AGTTCGGGGA GGGGGTAGCA CCCTGGTCTA CACCTTCACA AACTAAGCGG AGTTCGGGTG 3041

L H G P T P L L Y R L G A V Q N E I T L T H P V T K CCTCCATGG CCAACACCC TGCTATACAG ACTGGGCGCT GTTCAGAATG AAATCACCCT GACGCACCCA GTCACCAAAT GGAGGTACCC GGTTGTGGGG ACGATATGTC TGACCCGCGA CAAGTCTTAC TTTAGTGGGA CTGCGTGGGT CAGTGGTTTA **+**5

Y I M T C M S A D L E V V T S T W V L V G G V L A A L ACATCATGAC ATGCATGTGG GCCGCGTCCT GGCTGCTTTG TGTACTTG GCGCCGTCCT GGCTGCTTTG TGTACTACTG TACGTACAGC CGGCTGGACC TCCAGCAGTG CTCGTGGACC CACGAGCAAC +2 Y I M 3201

A A Y C L S T G C V V I V G R V V L S G K P A I I P D GCCGCGTATT GCCTGTCAAC AGGCTGCTG GTCATAGTGG GCAGGGTCGT CTTGTCCGGG AAGCCGGCAA TCATACCTGA CGGCCCATAA CGGACAGTTG TCCGACGCAC CAGTATCACC CGTCCCAGCA GAACAGGCCC TTCGGCCGTT AGTATGGACT +5 3281

GGGATGATGC CCCTACTACG R E V L Y R E F D E M E E C S Q H L P Y I E Q CAGGGAAGTC CTCTACCGAG AGTTCGATGA GATGGAAGAG TGCTCTCAGC ACTTACCGTA CATCGAGCAA GTCCTTCAG GAGATGGCTC TCAAGCTACT CTACCTTCTC ACGAGAGTCG TGAATGGCAT GTAGCTCTT +7 3361

+2 L A E Q F K Q K A L G L L Q T A S R Q A E V I A P A V il TCGCCGAGCA GTTCAAGCAG AAGGCCCTCG GCCTCCTGCA GACCGCGTCC CGTCAGGCAG AGGTTATCGC CCTGCTGTC AGCGGCTCGT CAAGTTCGTC TTCCGGGAGC CGGAGGACGT CTGGCGCAGG GCAGTCCGTC TCCAATAGCG GGGACGACAG

Q T N W Q K L E T F W A K H M W N F I S G I Q Y L A G CAGACCAACT GGCAAAAACT CGAGACCTTC TGGCGGAGC ATATGTGGAA CTTCATCAGT GGGATACAAT ACTTGGCGGG GTCTGGTTGA CCGTTTTTGA GCTCTGGAAG ACCCGCTTCG TATACACCTT GAAGTAGTCA CCCTATGTTA TGAACCGCC 3521

D V V V V A T D A L M T G Y T G D F D S V I D C N T C GATGTTGT TCGTGGCAAC CGATGCCCTC ATGACCGGCT ATACCGGCGA CTTCGACTCG GTGATAGACT GCAATACGTG CACTATCTGA CGTTATGCAC CTACAACAGC AGCACCGTTG GCTACGGGAG TACTGGCCGA TATGGCCGCT GAAGCTGAGC 2561

V T Q T V D F S L D P T F T I E T I T L P Q D A V S TGTCACCCCAG ACAGTCGATT TCAGCCTTGA CCCTACCTTC ACCATTGAGA CAATCACGCT CCCCCAAGAT GCTGTCTCCC ACAGTGGGTC TGTCAGCTAA AGTCGGAACT GGGATGGAACTCT GTTAGTGCGA GGGGGTTCTA CGACAGAGGG +2

+5 2721

M F D S S V L C E C Y D A G C A W Y E L T P A E T T V AIGTICGACT CGTCGTCG TATGACGCAG GCTCTGCTTG GTATGAGCTC ACGCCCGCCG AGACTACAGT TACAAGCTGA GCAGGCAGGA GACACTCACG ATACTGCGTC CGACACGAAC CATACTCGAG TCTGATGTCA 7 2801

Н G 口 3 1 Н H Ω 0 ပ > Д Н G д Н Z Σ ¥ Н ĸ +2

StuI

GTCTTTACAG CAGAAATGTC GCGTACATGA ACACCCCGGG GCTTCCCGTG TGCCAGGACC ATCTTGAATT TTGGGAGGGC CGCATGTACT TGTGGGGCGCC CGAAGGGCAC ACGGTCCTGG TAGAACTTAA AACCCTCCCG TTGGGAGGGC TAGGCTACGA ATCCGATGCT

2881

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GAGAACCTIC CTTACCTGGT AGCGTACCAA GAATGGACCA TCGCATGGTT CTCTTGGAAG GCAGAGTGGG CGTCTCACCC CACTITCIAI CCCAGACAAA ATATCTACGG GIGAAAGATA GGGICTGTTT TATAGATGCC CGGAGTGAGT GCCTCACTCA 2961

				DCN DCN	pCMV-NS35			
8961	CCCATGTTGT GGGTACAACA	GCAAAAAGC CGTTTTTTCG	GGTTAGCTCC CCAATCGAGG	TTCGGTCCTC AAGCCAGGAG	GGTTAGCTCC TTCGGTCCTC CGATCGTTGT CCAATCGAGG AAGCCAGGAG GCTAGCAACA	CAGAAGTAAG GTCTTCATTC	TTGGCCGCAG AACCGGCGTC	TGTTATCACT ACAATAGTGA
9041	CATGGTTATG GTACCAATAC	GCAGCACTGC CGTCGTGACG	ATAATTCTCT TATTAAGAGA	TACTGTCATG ATGACAGTAC	CCATCCGTAA GGTAGGCATT	GATGCTTTTC CTACGAAAAG	TGTGACTGGT ACACTGACCA	GAGTACTCAA CTCATGAGTT
9121	CCAAGTCATT GGTTCAGTAA	CTGAGAATAG GACTCTTATC	TGTATGCGGC ACATACGCCG	GACCGAGTTG	CTCTTGCCCG	GCGTCAATAC CGCAGTTATG	GGGATAATAC CCCTATTATG	CGCGCCACAT
9201	AGCAGAACTT TCGTCTTGAA	TAAAAGTGCT ATTTTCAGGA	CATCATTGGA GTAGTAACCT	AAACGTTCTT TTTGCAAGAA	CGGGGCGAAA	ACTCTCAAGG TGAGAGTTCC	ATCTTACCGC TGTTGAGATC TAGAATGGCG ACAACTCTAG	TGTTGAGATC
9281	CAGTTCGATG GTCAAGCTAC	TAACCCACTC ATTGGGTGAG	GTGCACCCAA CACGTGGGTT	CTGATCTTCA GACTAGAAGT	GCATCTTTTA	CTTTCACCAG	CGTTTCTGGG	TGAGCAAAAA ACTCGTTTTT
9361	CAGGAAGGCA GTCCTTCCGT	CAGGAAGGCA AAATGCCGCA GTCCTTCCGT TTTACGGCGT	AAAAAGGGAA TTTTTCCCTT	TAAGGGGGAC ATTCCCGCTG	ACGGAAATGT TGCCTTTACA		TACTCTTCCT ATGAGAAGGA	TTTTCAATAT AAAAGTTATA
9441	TATTGAAGCA ATAACTTCGT	TATTGAAGCA TTTATCAGGG ATAACTTCGT AAATAGTCCC	TTATTGTCTC AATAACAGAG	ATGAGCGGAT TACTCGCCTA	ACATATTTGA ATGTATTTAG AAAAATAAAC AAATAGGGGT TGTATAAACT TACATAAATC TTTTTATTTG TTTATCCCCA	ATGTATTTAG TACATAAATC	AAAAATAAAC TTTTTATTTG	AAATAGGGT TTTATCCCCA
9521	TCCGCGCACA	TCCGCGCACA TTTCCCCGAA AGGCGCGTGT AAAGGGGCTT	AAGTGCCACC TTCACGGTGG	TGACGTCTAA ACTGCAGATT	GAAACCATTA CTTTGGTAAT	TTATCATGAC AATAGTAG	ATTAACCTAT TAATTGGATA	AAAAATAGGC TTTTTATCCG
9601	GTATCACGAG CATAGTGCTC	GCCCTTTCGT CGGGAAAGCA	ပဗ					

FIG. 3-Page 16

8241	AGGACAGTAT TCCTGTCATA	TTGGTATCTG	CGCTCTGCTG GCGAGACGAC	AAGCCAGTTA TTCGGTCAAT	CCTTCGGAAA	AAGAGTTGGT TTCTCAACCA	AGCTCTTGAT TCGAGAACTA	CCGGCAAACA GGCCGTTTGT
8321	AACCACCGCT TTGGTGGCGA	GGTAGCGGTG . CCATCGCCAC	GTTTTTTGT TTGCAAGCAG CAAAAAACA AACGTTCGTC	TTGCAAGCAG AACGTTCGTC	CAGATTACGC GTCTAATGCG	GCAGAAAAA	AGGATCTCAA TCCTAGAGTT	GAAGATCCTT CTTCTAGGAA
8401	TGATCTTTTC ACTAGAAAG	TACGGGGTCT ATGCCCCAGA	GACGCTCAGT CTGCGAGTCA	GGAACGAAAA CCTTGCTTTT	CTCACGTTAA GAGTGCAATT	GGGATTTTGG	TCATGAGATT AGTACTCTAA	ATCAAAAAGG TAGTTTTCC
8481	ATCTTCACCT TAGAAGTGGA	AGATCCTTTT TCTAGGAAAA	AAATTAAAAA TTTAATTTTT	TGAAGTTTTA ACTTCAAAAT	AATCAATCTA TTAGTTAGAT	AAGTATATAT TTCATATATA	GAGTAAACTT CTCATTTGAA	GGTCTGACAG
8561	TTACCAATGC AATGGTTACG	TTAATCAGTG AATTAGTCAC	AGGCACCTAT TCCGTGGATA	CTCAGCGATC	TGTCTATTTC ACAGATAAAG	GTTCATCCAT CAGE	AGTTGCCTGA TCAACGGACT	CTCCCCGTCG
8641	TGTAGATAAC ACATCTATTG	TGTAGATAAC TACGATACGG ACATCTATTG ATGCTATGCC	GAGGGCTTAC CTCCCGAATG	CATCTGGCCC GTAGACCGGG	CAGTGCTGCA GTCACGACGT	ATGATACCGC (GAGACCCACG	CTCACCGGCT
8721	CCAGATTTAT GGTCTAAATA	CCAGATTTAT CAGCAATAAA GGTCTAAATA GTCGTTATTT	CCAGCCAGCC GGTCGGTCGG	GGAAGGGCCG	AGCGCAGAAG TCGCGTCTTC	TGGTCCTGCA A	ACTTTATCCG TGAAATAGGC	CCTCCATCCA
8801	GTCTATTAAT CAGATAATTA	TGTTGCCGGG ACAACGGCCC	AAGCTAGAGT TTCGATCTCA	AAGTAGTTCG TTCATCAAGC	CCAGTTAATA	GTTTGCGCAA (CGTTGTTGCC /	ATTGCTACAG TAACGATGTC
8881	GCATCGTGGT CGTAGCACCA	GTCACGCTCG CAGTGCGAGC	TCGTTTGGTA AGCAAACCAT	TGGCTTCATT ACCGAAGTAA	CAGCTCCGGT GTCGAGCCA	TCCCAACGAT C	CAAGGCGAGT GTTCCGCTCA	TACATGATCC

FIG. 3-Page 15

oCMV-NS35

7521	CGCATTGTCT GCGTAACAGA	GAGTAGGTGT CTCATCCACA	CATTCTATTC	pCMV- regegegree Acccccacc	pCMV-NS35 TGGGGGTGG GGTGGGGCAG ACCCCCACC CCACCCGTC	GACAGCAAGG CTGTCGTTCC	GGGAGGATTG CCCTCCTAAC	GGAAGACAAT CCTTCTGTTA
7601	AGCAGGCATG TCGTCCGTAC	CTGGGGAGCT GACCCCTCGA	CTTCCGCTTC GAAGGCGAAG	CTCGCTCACT	GACTCGCTGC CTGAGCGACG	GCTCGGTCGT	TCGGCTGCGG	CGAGCGGTAT
7681	CAGCTCACTC GTCGAGTGAG	AAAGGCGGTA TTTCCGCCAT	ATACGGTTAT TATGCCAATA	CCACAGAATC	AGGGGATAAC TCCCCTATTG	GCAGGAAAGA	ACATGTGAGC TGTACACTCG	AAAAGGCCAG TTTTCCGGTC
7761	CAAAAGGCCA GTTTTCGGGT	CAAAAGGCCA GGAACCGTAA GTTTTCCGGT CCTTGGCATT	AAAGGCCGCG TTTCCGGCGC	TTGCTGGCGT	TTTTCCATAG AAAAGGTATC	GCTCCGCCCC	CCTGACGAGC	ATCACAAAAA TAGTGTTTTT
7841	TCGACGCTCA AGCTGCGAGT	TCGACGCTCA AGTCAGAGGT AGCTGCGAGT TCAGTCTCCA	GGCGAAACCC CCGCTTTGGG	GACAGGACTA CTGTCCTGAT	TAAAGATACC ATTTCTATGG	AGGCGTTTCC TCCGCAAAGG	CCCTGGAAGC	TCCCTCGTGC
7921	GCTCTCCTGT CGAGAGGACA	GCTCTCCTGT TCCGACCCTG CGAGAGGACA AGGCTGGGAC	CCGCTTACCG GCCGAATGGC	GATACCTGTC CTATGGACAG	CGCCTTTCTC	CCTTCGGGAA GGAAGCCCTT	GCGTGGCGCT CGCACCGCGA	TTCTCAATGC
8001	TCACGCTGTA AGTGCGACAT	GGTATCTCAG CCATAGAGTC	TTCGGTGTAG AAGCCACATC	GTCGTTCGCT	CCAAGCTGGG	CTGTGTGCAC	GAACCCCCG	TTCAGCCCGA
8081	CCGCTGCGCC GGCGACGCGG	TTATCCGGTA AATAGGCCAT	ACTATCGTCT TGATAGCAGA	TGAGTCCAAC ACTCAGGTTG	CCGGTAAGAC	ACGACTTATC TGCTGAATAG	GCCACTGGCA	GCAGCCACTG
8161	GTAACAGGAT CATTGTCCTA	TAGCAGAGCG ATCGTCTCGC	AGGTATGTAG TCCATACATC	GCGGTGCTAC AGAGTTCTTG CGCCACGATG TCTCAAGAAC		AAGTGGTGGC (CTAACTACGG (GATTGATGCC)	CTACACTAGA GATGTGATCT

FIG. 3-Page 14

D A E S Y S M P P GACGCTGAGT CCTATTCCTC CATGCCCCC GGGGGGGAA GACCGACGGG GGGGCTGAGG CTGCGACTCA GGATAAGGAG GTACGGGGGG P A P S G C P P D S CCCGCCCTT CTGGCTGCC CCCCGACTCC ATACGACAAC ATCCTCTGAG TATGCTGTTG TAGGAGACTC ഥ 5361

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GAGGCCAACG CGGAGGATGT CTCCGGTTGC GCCTCCTACA AGCGACGGGT CATGGTCAAC GGTCAGTAGT TCGCTGCCCA GTACCAGTTG CCAGTCATCA CTGGAGGGG AGCCTGGGGA TCCGGATCTT GACCTCCCC TCGGACCCCT AGGCCTAGAA 5441

CGTGTGCTGC TCAATGTCTT ACTCTTGGAC AGGCGCACTC GTCACCCGGT GCGCGGGGA AGAACAGAAA CTGCCCATCA GCACACGACG AGTTACAGAA TGAGAACCTG TCCGCGTGAG CAGTGGGGCA CGCGGCGCCT TCTTGTCTTT GACGGTAGT Þ A E A V T P C SWT × S , ပ

N A L S N S L L R H H N L V Y S T T S R S A C Q R Q K ATGCACTAAG CAACTCGTTG CTACGTCAC AGGCAGAAG TACGTGATTC GTTGAGCAAC GTGCAGGTG TGTTAAACCA CATAAGGTG TGGAGTGC TGCAGGTG TGCAGTGT TTCCGTCTTC N A L S N S L ATGCACTAAG CAACTCGTTG 5601

K V T F D R L Q V L D S H Y Q D V L K E V K A A A S K AAAGTCACAT TTGACAGACT GCAAGTTCTG GACAGCCATT ACCAGGACGT ACTCAAGGAG GTTAAAGCAG CGGCGTCAAA TTTCAGTGTA AACTGTCTGA CGTTCAAGGAC CTGTCGGTAA TGGTCCTGCA TGAGTTCCTC CAATTTCGTC GCGCAGTTTT +5 5681

V K A N L L S V E E A C S L T P P H S A K S K F G Y AGTGAAGGCT AACTIGCTAT CCGTAGAGGA AGCTTGCAGC CTGACGCCC CACACTCAGC CAAATCCAAG TTTGGTTATG TCACTTCCGA TTGAACGATA GGCATCTCCT TCGAACGTCG GACTGCGGGG GTGTGAGTCG GTTTAGGTTC AAACCAATAC 5761

AGACACCGGG TCTGTGGCCC E I N R V A A C L R K L G V P P L R W W GAAATCAATA GGGTGGCGG ATGCCTCAGA AAACTTGGG TACCGCCCTT GCGAGCTTGG TTTAGTTAT CCCACCGGCG TACGGAGTCT TTTGAACCCC ATGGCGGGAA CGCTCGAACC CTCTCCAGGT GAGAGGTCCA Ъ

A R S V R A R L L A R G G R A I C G K Y L F N W A V CCCGGAGCGT CCGCGCTAGG CTTCTGGCCA GAGGAGGCAG GGCTGCCATA TGTGGCAAGT ACCTCTTCAA CTGGGCAGTA GGCCCTCGCA GGCGCGATCG GAGGCCGTC CCGACGTAT ACACCGTTCA TGGAGAAGTT GACCCGTCAT +5 7041

R T K L K L T P I A A A G Q L D L S G W F T A G Y S G AGAACAAAGC TCAAACTCAC TCCAATAGCG GCCGCTGGCTGGCTT GTCCGGCTGG TTCACGGCTG GCTACAGCGG TCTTGTTTCG AGTTTGAGTG AGGTTATCGC CGCCGACCGG TCGACCTGAA CAGGCCGACC AAGTGCCGAC CGATGTCGCC + 7121

G D I Y H S V S H A R P R W I W F C L L L A A G V GGGAGACATT TATCACAGCG TGTCTCATGC CCGGCCCGG TGGATCTGGT TTTGCCTACT CCTGCTTGCT GCAGGGGTAG CCCTCTGTAA ATAGTGTCGC ACAGAGTACG GGCCCGGGCG ACCTAGACCA AAACGGATGA GGACGAACGA CGTCCCCATC

AAAGGCGCGC TTTCCGCGCGC AAAAATCTAG TTTTAGATC G I Y L L P N R GCATCTACCT CCTCCCCAAC GGATGAAGGT TGGGGTAAAC ACTCCGGCCT AAAAAAAAA CGTAGATGGA GGAGGGGTTG GCTACTTCCA ACCCCATTTG TGAGGCCGGA TTTTTTTTT

BAMHI MluI

GTAGACAACA CATCTGTTGT CAGCCTCGAC TGTGCCTTCT AGTTGCCAGC GTCGGAGCTG ACACGGAAGA TCAACGGTCG GCTCGCTGAT CGAGCGACTA ACGCGTTAGA TGCGCAATCT AGGATCCACT TCCTAGGTGA CAAGATATCA GTTCTATAGT

CTTTAACGTA GGAAGGTGCC ACTCCCACTG TCCTTTCCTA ATAAATGAG CCTTCCACGG TGAGGGTGAC AGGAAAGGAT TATTTTACTC GGAACTGGGA CCTTGACCCT CCCGTGCCTT GGGCACGGAA AACGGGGAGG TIGCCCCTCC 7441

N T L T C Y I K A R A A C R A A G L Q D C T M L V C G AACACCCTCA CITGCTACAT CAAGGCCCGG GCAGCCTGTC GAGCCGCAGG GCTCCAGGAC TGCACCATGC TCGTGTGTGG TTGTGGGAGT GAACGATGTA GTTCCGGGCC CGTCGGACAG CTCGGCGTCC CGAGGTCCTG ACGTGGTACG AGCACACACC +2 6401

D D L V V I C E S A G V Q E D A A S L R A F T E A M CGACGACTTA GTCGTTATCT GTGAAAGGGC GGGGGTCCAG GAGGACGCGG CGAGCCTGAG AGCCTTCACG GAGGCTATGA GCTGCTGAAT CAGCAATAGA CACTTTCGCG CCCCCAGGTC CTCCTGCGCC GCTCGGACTC TCGGAAGTGC CTCCGATACT +2

T R Y S A P P G D P P Q P E Y D L E L I T S C S S N V CCAGGIACTC CCCCCCCCT GGGGACCCC CACAACCAGA ATACGACTTG GAGCTCATAA CATCATGCTC CTCCAACGTG GGTCCATGAG GCGGGGGGGA CCCTGGGGG GTGTTGGTCT TATGCTGAAC CTCGAGTATT GTAGTACGAG GAGGTTGCAC

S V A H D G A G K R V Y Y L T R D P T T P L A R A A W TCAGTCGCC ACGACGCC TGGAAAGAG GTCTACTACC TCACCCGTGA CCCTACAACC CCCCTCGCGA GAGCTGCGTG AGTCAGCGGG TGCTGCCGC ACCTTTCTCC CAGATGATGG AGTGGGCACT GGGATGTTGG GGGAGCGCT CTCGACGCAC 6641

GCGAGGATGA CGCTCCTACT E T A R H T P V N S W L G N I I M F A P T L W GGAGACAGCA AGACACACTC CAGTCAATTC CTGGCTAGGC AACATAATCA TGTTTGCCCC CACACTGTGG CCTCTGTGTGAG GTCAGTTAAG GACCGATCCG TTGTATTAGT ACAAACGGGG GTGTGACACC 6721

I L M T H F F S V L I A R D Q L E Q A L D C E I Y G A TACTEGATEGAT CACTEGATEGAT CTACGGGGCC ATGCCAGAT CTACGGGGCC ATGACTAAGAAA TCGCAGAAT ATCGCTCCT GGTCCAACTT GTCCGGGAGC TAACGCTCTA GATGCCCCGG

C Y S I E P L D L P P I I Q R L H G L S A F S L H S Y TGCTACTCCA TAGAACCACT GGATCTACCT CCACAGTTA ACGATGAGGT ACGAGGGT ATCTTGGTGA CCTAGATGGA GGTTAGTAAG TTTCTGAGGT ACCGGAGTCG CGTAAAAGTG AGGTGTCAAT 6881

I T A E A A G R R L A R G S P P S V A S S A ATAACAGCAG AGGGGGGTG GCGAGGTTG GCGAGGGGAT CACCCCCTC TGTGGCCAGC TCCTCGGCTA TATTGTCGTC TCCGCCGGCC CGCTTCCAAC CGCTCCCCTA GTGGGGGGAG ACACCGGTCG AGGAGCCGAT TCCCTCCCAT AGGGAGGGTA 4801

S Q L S A P S L K A T C T A N H D S P D A E L I E A N GCCAGCTATC CGCTCCATCT CTCAAGGCCAA CTTGCACGC TAACCATGAC TCCCCTGATG CTGAGCTCAT AGAGGCCAAC CGGTCGATAG GCGAGGTAGA GAGTTCCGTT GAACGTGGCG ATTGGTACTG AGGGGACTAC GACTCGAGTA TCTCCGGTTG 4881

L L W R Q E M G G N I T R V E S E N K V V I L D S F D CTCCTATGGA GGCAGGAGAT GGGCGGCAAC ATCACCAGG TTGAGTCAGA AAACAAAGTG GTGATTCTGG ACTCCTTCGA GAGGATACCT CCGTCCTCTA CCGCCGTTG TAGTGGTCCC AACTCAGTCT TTTGTTTCAC CACTAAGACC TGAGGAAGCT +5

P L V A E E D E R E I S V P A E I L R K S R F F A Q TCCGCTTGTG GCGGAGGAGG ACGAGCGGGA GATCTCCGTA CCCGCAGAAA TCCTGCGGAA GTCTCGGAGA TTCGCCCAGG AGGCGAACAC GGCCTCCTCC TGCTCGCCCT CTAGAGGCAT GGGCGTCTTT AGGACGCCTT CAGAGCCTCT AAGCGGGTCC

CCCTGCCCGT TTGGGCGCGG CCGGACTATA ACCCCCGGT AGTGGAGGG TGGAAAAAGC CCGACTACGA ACCACCTGTG GGGACGGGCA AACCCGCGCC GGCCTGATAT TGGGGGGCGA TCACCTCTGC ACCTTTTTCG GGCTGATGCT TGGTGGACAC A Q W K K P ĿΊ P P L P D Y N A R 3 A L P V

V H G C P L P P K S P P V P P P R K K K R T V V L T E GICCAIGGCI GCCGCTICC ACTCCAAAG TCCCCTCTG TGCCTCCGC TCGGAAGAAG CGGACGGTGG TCCTCACTGA CAGGTACCGA CGGGCGAAGG TGGAGGTTTC AGGGGAGGAC ACGGAGGCGG AGCCTTCTTC GCCTGCCACC AGGAGTGACT 5201

S T L S T A L A E L A T R S F G S S T S G I T G D ATCAACCCTA TCTACTGCCT TGGCGGGGGT GGCCACAGA AGCTTTGGCA GCTCCTCAAC TTCCGGCATT ACGGGCGACA TAGTTGGGAT AGATGACGGA ACCGGCTCGA GCGGTGGTCT TCGAAACCGT CGAGGAGTTG AAGGCCGTAA TGCCCGCTGT

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GGTATAAGGG CCATATTCCC TGCCAGCGCG ACGGTCGCGC CCACAGCTGC CTGGGATCCC CTTTGTGTCC GGTGTCGACG GACCCTAGGG GAAACACAGG TAAGCTCATG AAATICIGGA CCGATITICG ATICGAGTAC GGCTAAAAGC TTTAAGACCT 4241

AACGGGACGA TTGCCCTGCT ტ z G D G I M H T R C H C G A E I T G H V K GGGGACGGCA TCATGCACAC TCGCTGCAC TGTGGAGCTG AGATCACTGG ACATGTCAAA CCCCTGCCGT AGTACGTGTG AGCGACGGTG ACACCTCGAC TCTAGTGACC TGTACAGTTT GGTCTGGCGA CCAGACCGCT 3 > 4321

M R I V G P R T C R N M W S G T F P I N A Y T T G P C TGAGGATCGT CGGTCCTAGG ACCTGCAGGA ACATGTGGAG TGGGACCTTC CCCATTAATG CCTACACCAC GGGCCCTGT ACTCCTAGCA GCCAGGATCC TGGACGTCCT TGTACACCTC ACCCTGGAAG GGGTAATTAC GGATGTGGTG CCCGGGGACA 4401

GTGGAGATAA GGCAGGTGGG CACCTCTATT CCGTCCACCC > Ŀì T P L P A P N Y T F A L W R V S A E E Y ACCCCCCTTC CTGCGCGAA CTACACGTTC GCGCTATGGA GGGTGTCTGC AGAGGAATAC (TGGGGGAAG GACGCGGCTT GATGTGCAAG CGCGATACCT CCCACAGACG TCTCCTTATG

D F H Y V T G M T T D N L K C P C Q V P S P E F F T GGACTTCCAC TACGTGACGG GTATGACTAC TGACAATCTT AAATGCCCGGT GCCAGGTCCC ATCGCCCGAA TTTTTCACAG CCTGAAGGTG ATGCACTGCC CATACTGATG ACTGTTAGAA TTTACGGGCA CGGTCCAGGG TAGCGGGCTT AAAAAGTGTC 4561

H R F A P C K P L L R E E V S F R V G CATAGGTITG CGCCCCCTG CAAGCCCTTG CTGCGGGGG AGGTATCAIT CAGAGTAGGA GTATCCAAAC GCGGGGGGGG GTTCGGGAAC GACGCCCTCC TCCATAGTAA GTCTCATCCT TTAACCTGCC CCACGCGGAT AATIGGACGG GGTGCGCCTA Н > G Ω +2 4641

CTCCACGAAT ACCCGGTAGG GTCGCÀATTA CCTTGCGAGC CCGAACGGGA CGTGGCCGTG TTGACGTCCA TGCTCACTGA GAGGTGCTTA TGGGCCATCC CAGCGTTAAT GGAACGCTCG GGCTTGGCCT GCACCGGCAC AACTGCAGGT ACGAGTGACT A V 1 0 Ç > 4721

S Q T L L F N I L G G W V A A Q L A P G A A T A F V GCCAAACCT CCTCTTCAAC ATATTGGGG GGTGGGTGGC TGCCCAGCTC GCCGCCCCCG GTGCCGTAC TGCCTTTGTG CGGTTTGGGA GGAGAAGTTG TATAACCCCC CCACCCACCG ACGGGTTCGAG CGGCGGGGC CACGGCGATG ACGGAAACAC 3681

G A G L A G A A I G S V G L G K V L I D I L A G Y G A GCCCTGCTGCT TAGCTGCGC CGCCATCGC AGTGTTGGAC TGGGGAAGGT CCTCATAGAC ATCCTTGCAG GGTATGGCGC CGCGACCGA ATCGACGCG GCGTAGCCG TCACAACCTG ACCCCTTCCA GGAGTATCTG TAGGAACGTC CCATACCGCG 3761

G V A G A L V A F K I M S G E V P S T E D L V N L L GGGCGTGGCG GGAGCTCTTG TGGCATTCAA GATCATGAGC GGTGAGGTCC CCTCCACGGA GGACCTGGTC AATCTACTGC CCCGCACCGC CCTCGAGAAC ACCGTAAGTT CTAGTACTCG CCACTCCAGG GGAGGTGCCT CCTGGACCAG TTAGATGACG

CCGCCATCCT CTCGCCCGGA GCCCTCGTAG TCGGCGTGGT CTGTGCAGCA ATACTGCGCC GGCACGTTGG CCCGGGCGAG GGCGGTAGGA GAGCGGGCCT CGGGAGCATC AGCCGCACCA GACACGTCGT TATGACGCGG CCGTGCAACC GGGCCCGCTC 24 I I A V ပ G V V A L V V Ç Д လ +5 3921

G A V Q W M N R L I A F A S R G N H V S P T H Y V P E GGGCAGTGC AGTGGATGAA CCGGCTGATA GCCTTCGCCT CCCGGGGGAA CCATGTTTCC CCCACGCACT ACGTGCCGGA CCCCGTCACG TCACCTACTT GGCGACTAT CGGAAGCGGA GGGCCCCTT GGTACAAAGG GGGTGCGTGA TGCACGGCCT 4001

A A R V T A I L S S L T V T Q L L R R L H Q W GCTGCCGCG TCACTGCCAT ACTCAGCAGC CTCACTGTAA CCCAGCTCCT GAGGCGACTG CACCAGTGGA CGACGGGCGC AGTGACGTA TGAGTCGTCG GAGTGACATT GGGTCGAGGA CTCCGCTGAC GTGGTCACCT GAGCGATGCA ¥ လ 4081

I S S E C T T P C S G S W L R D I W D W I C E V L S D TAAGCTCGGA GTGTACCACT CCATGCTCGG GTTCCTGGCT AAGGGACATC TGGGACTGGA TATGCGAGGT GTTGAGCGACAGACTG CAAGGACCGA TTCCCTGTAG ACCCTGACCT ATACGCTCCA CAACTCGCTG 4161

L H G P T P L L Y R L G A V Q N E I T L T H P V T K CCTCCATGG CCAACACCCC TGCTATACAG ACTGGGCGCT GTTCAGAATG AAATCACCCT GACGCACCCA GTCACCAAT GGAGGTACCC GGTTGTGGGG ACGATATGTC TGACCCGCGA CAAGTCTTAC TTTAGTGGGA CTGCGTGGGT CAGTGGTTTA 3121

Y I M T C M S A D L E V V T S T W V L V G G V L A A L ACATCATGAC ATGCATGTG GCGACCTGG AGGTCGTCAC GAGCACCTGG GTGCTTG GCGCGTCCT GCTGCTTTG TGTAGTACTG TACGTACAGC CGGCTGGACC TCCAGCAGTG CTCGTGGACC CACGAGCAAC +5 3201

A A Y C L S T G C V V I V G R V V L S G K P A I I P D GCCGCCTATT GCCTCTCAAC AGGCTGGTG GTCATAGTGG GCAGGGTCGT CTTGTCCGGG AAGCCGGCAA TCATACCTGA CGGCGCATAA CGGACAGTTG TCCGACGCAC CAGTATCACC CGTCCCAGCA GAACAGGCCC TTCGGCCGTT AGTATGGACT +5

L Y R E F D E M E E C S Q H L P Y I E Q G M M CTCTACCGAG AGTTCGATGA GATGGAAGAG TGCTCTCAGC ACTTACCGTA CATCGAGCAA GGGATGATGC GAGATGGCTC TCAAGCTACT CTACCTTCTC ACGAGAGTCG TGAATGGCAT GTAGCTCGTT CCCTACTACG CAGGGAAGTC GTCCCTTCAG Ħ

F K Q K A L G L L Q T A S R Q A E V I A P A V GTTCAAGCAG AAGGCCCTCG GCCTCCTGCA GACCGCGTCC CGTCAGGCAG AGGTTATCGC CCCTGCTGTC CAAGTTCGTC TTCCGGGAGC CGGAGGACGT CTGGCGCAGG GCAGTCCGTC TCCAATAGCG GGGACGACAG $oldsymbol{ ext{L}}$ A $oldsymbol{ ext{E}}$ Q $oldsymbol{ ext{TCGCCGAGCA}}$ AGCGCCTCGT 3441

Q T N W Q K L E T F W A K H M W N F I S G I Q Y L A G CAGACCAACT GGCAAAACT CGAGACCTTC TGGGCGAAGC ATATGTGGAA CTTCATCAGT GGGATACAAT ACTTGGCGGG GTCTGGTTGA CCGTTTTGA GCTCTGGAAG ACCCGCTTCG TATACACCTT GAAGTAGTCA CCCTATGTTA TGAACCGCCC +5 3521

L S T L P G N P A I A S L M A F T A A V T S P L T T CTTGTCAACG CTGCCTGGTA ACCCCGCCAT TGCTTCATTG ATGCTTTTA CAGCTGCTGT CACCAGCCCA CTAACCACTA GAACAGTTGC GACGGACCAT TGGGGCGGTA ACGAAGTAAC TACCGAAAAT GTCGACGACA GTGGTCGGGT GATTGGTGAT 3601

V T Q T V D F S L D P T F T I E T I T L P Q D A V S TGTCACCCAG ACAGTCGATT TCAGCCTTGA CCCTACCTTC ACCATTGAGA CAATCACGCT CCCCCAAGAT GCTGTCTCCC ACAGTGGGTC TGTCAGCTAA AGTCGGAACT GGGATGGAAG TGGTAACTCT GTTAGTGCGA GGGGGTTCTA CGACAGAGGG 2641

F V A P G E R P S G TTTGTGGCAC CGGGGAGG AAACACGGTG GCCCCTCGC GGGGAGGCCG GCACTCÀACG TCGGGGCAGG ACTGGCAGGG GGAAGCCAGG CATCTACAGA CGTGAGTTGC AGCCCGTCC TGACCGTCC CCTTCGGTCC GTAGATGTCT × G × G ĸ G R T Q R R G R GCACTCAACG TCGGGGCAGG 2721

M F D S S V L C E C Y D A G C A W Y E L T P A E T T V ATGTTCGACT CGTCCGTCCT CTGTGAGTGC TATGACGCAG GCTGTGCTTG GTATGAGCTC ACGCCCGCG AGACTACAGT TACAAGCTGA GCAGGCAGGA GACACTCACG ATACTGCGTC CGACACGAAC CATACTCGAG TGCGGGCGGC TCTGATGTCA 2801

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StuI TTGGGAGGGC AACCCTCCCG TAGAACTTAA TGCCAGGACC ATCTTGAATT ACGGTCCTGG GCTTCCCGTG CGAAGGGCAC ACACCCCGGG TGTGGGGCCC GCGTACATGA CGCATGTACT TAGGCTACGA ATCCGATGCT 2881

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GAGAACCTTC CTTACCTGGT AGCGTACCAA CTCTTGGAAG GAATGGACCA TCGCATGGTT GAGAACCTTC GCAGAGTGGG CGTCTCACCC CACTITCIAI CCCAGACAAA GTGAAAGATA GGGTCTGTTT CGGAGTGAGT ATATCTACGG GCCTCACTCA TATAGATGCC 2961

GGGGGTAGCA CCCTGGTCTA CACCTTCACA AACTAAGCGG AGTTCGGGTG 3041

Ç ATCACGTACT CCACCTACGG TAGTGCATGA GGTGGATGCC S G V R T I T G S P GGGTGAGAA CAATTACCAC TGGCAGCCCC CCCCACTCTT GTTAATGGTG ACCGTCGGGG GCTCATGGGA TCGATCCTAA CATCAGGACC CGAGTACCCT AGCTAGGATT GTAGTCCTGG ტ

K F L A D G G C S G G A Y D I I C D E C H S T D A CAAGTICCIT GCCACGGCG GGIGCICGGG GGGCGCTTAT GACATAALATIGIGACGA GIGCCACTCC ACGGAIGCCA GITCAAGGAA CGGCIGCCGC CCCGCGAAIA CIGIAITAIT AAACACIGCT CACGGIGAGG IGCCIACGGI 2161

T S I L G I G T V L D Q A E T A G A R L V V L A T A T A C A R L V V L A T A T CATCCATCTT GGCCATTGGC ACTGTCCTTG ACCAAGCAGA GACTGCGGG GCGAGACTGG TTGTGCTCGC CACCGCCACC GTAGGTAGAA CCCGTAACCG TGACGGAAC TGGTTCGTCT CTGACGCCC CGCTCTGACC AACACGAGGG GTGGCGGTGG 2241

+2 2321

K A I P L E V I K G G R H L I F C H S K K C D E L CAAGGCTATC CCCTCGAAG TAATCAAGGG GGGGAGACAT CTCATCTTCT GTCATTCAAA GAAGAAGTGC GACGAACTCGGTTCCGATAG GGGGAGCTTC ATTAGTTCCC CCCCTCTGTA GAGTAGAAGA CAGTAAGTTT CTTCTTCACG CTGCTTGAGG +

GGCATCAATG CCGTGGCCTA CTACCGCGGT CTTGACGTGT CCGTCATCCC GACCAGCGGC CCGTAGTTAC GGCACCGGAT GATGGCGCCCA GAACTGCACA GGCAGTAGGG CTGGTCGCCG > L D ტ 2 × Ą > ¥ z ტ A A K L V A CGCGCATTG GC 2481

D V V V V A T D A L M T G Y T G D F D S V I D C N T C GATGITGICG TCGTGCCAC CGATGCCTC ATGACCGGCT ATACCGGCGA CITCGACTCG GTGATAGACT GCAATACGTG CTACAACAGC AGCACCGTTG GCTACGGGGAG TACTGGCCGCT GAAGCTGAGC CACTATCTGA CGTTATGCAC + 2561

DCMV-NS35

1441	TATTTACAAA ATAAATGTTT	A TTCACATATA T AAGTGTATAT	A CAACAACGCC I GTTGTTGCGG	GTCCC	PCMV-NS35 CGTG CCGGCAGTTT GGCAC GGGCGTCAAA	TTATTAAACA AATAATTTGT	TAGCGTGGGA ATCGCACCCT	TCTCCGACAT AGAGGCTGTA
1521	CTCGGGTAC	CTCGGGTACG TGTTCCGGAC GAGCCCATGC ACAAGGCCTG	ATGGGCTCTT TACCCGAGAA	CTCCGGTAGC	GGGGGAGCTT	CCACATCCGA	GCCCTGGTCC	
1601	GCGGCTCATG CGCCGAGTAC	G GTCGCTCGCC C CAGCGAGCCG		AGCTCCTTGC TCCTAACAGT TCGAGGAACG AGGATTGTCA	GGAGGCCAGA	CTTAGGCACA GAATCCGTGT	GCACAATGCC	CACCACCACC
1681	AGTGTGCCGC TCACACGGCG	AGTGTGCGGC ACAAGGCCGT TCACACGGCG TGTTCCGGCA	GGCGGTAGGG CCGCCATCCC	TATGTGTCTG ATACACAGAC	AAAATGAGCT TTTTACTCGA	CGGAGATTGG	GCTCGCACCT	GGACGCAGAT
1761	GGAAGACTTA CCTTCTGAAT	AGGCAGCGC	AGAAGAAGAT TCTTCTTCTA	GCAGGCAGCT	GAGTTGTTGT CTCAACAACA	ATTCTGATAA TAAGACTATT	GAGTCAGAGG	TAACTCCCGT
1841	TGCGGTGCTG ACGCCACGAC	TGCGGTGCTG TTAACGGTGG ACGCCACGAC AATTGCCACC	AGGGCAGTGT TCCCGTCACA	AGTCTGAGCA TCAGACTCGT	GTACTCGTTG	CTGCCGCGCG	CGCCACCAGA	CATAATAGCT GTATTATCGA
+2								
1921	GACAGACTAA CTGTCTGATT	CAGACTGTTC GTCTGACAAG	CTTTCCATGG (GTCTTTCTG CAGAAAAGAC	CAGTCACCGT GTCAGTGGCA	CGTCGACCTA 4	EcoRI AGAATTCACC TCTTAAGTGG	M A A ATGGCTGCAT TACCGACGTA
+2 2001	Y A A Q ATGCAGCTCA TACGTCGAGT	Y A A Q G Y K ATGCAGCTCA GGGCTATAAG TACGTCGAGT CCCGATATTC	V L V L N P S V A A T L G F G A Y M S K GTGCTAGTAC TCAACCCCTC TGTTGCTGCA ACACTGGGCT TTGGTGCTTA CATGTCCAAG CACGATCATG AGTTGGGGAG ACAACGACGT TGTGACCCGA AACCACGAAT GTACAGGTTC	N P S ICAACCCTC	V A A T TGTTGCTGCA A	T L G F ACACTGGGCT I	G A Y TGGTGCTTA ACCACGAAT	M S K CATGTCCAAG GTACAGGTTC

FIG. 3-Page 3

- V R C H A R K A V T H I N S V W K D L L E D N CGTCCGTTGC CATGCCAGAA AGGCCGTAAC CCACATCAAC TCCGTGTGGA AAGACCTTCT GGAAGACAAT GCAGGCAACG GTACGGTCTT TCCGGCATTG GGTGTAGTTG AGGCACACCT TTCTGGAAGA CCTTCTGTTA CCGTTTTCT GCAGGCAACG GGGCAAAAGA A 5841
- V T P I D T T I M A K N E V F C V Q P E K G G R K P A GTAACACCAGC TTTTCTGCGT TCAGCCTGAG AAGGGGGGTC GTAAGCCAGC CATTGTGCTG TTTTTTTTGTGCT AGGCGGGTC GTAAGCCAGC CATTGTGCTCC AAAAGACGCA AGTCGGACTC TTCCCCCCAG CATTCGGTCG 5921
- R L I V F P D L G V R V C E K M A L Y D V V T K L P TCGTCTCATC GTGTTCCCCG ATCTGGGCGT GCGCGTGTGC GAAAGATGG CTTTGTACGA CGTGGTTACA AAGCTCCCCT AGCAGAGTAG CACAAGGGGC TAGACCCGCA CGCGCACACG CTTTTCTACC GAAACATGCT GCACCAATGT TTCGAGGGGA
- 3 A 0 ഠ 卍 0 Ç Д S \succ 0 Γ4 G S တ S Σ \triangleright ď Ц

S

EcoRI

- GTGGAAGTCC CACCTTCAGG TCGTGCAAGC CAACTTAAGG AGCACGTTCG GTTGAATTCC TGGCCGTGAT GGGAAGCTCC TACGGATTCC AATACTCACC AGGACAGCGG ACCGGCACTA CCCTTCGAGG ATGCCTAAGG TTATGAGTGG TCCTGTCGCC TGGCCGTGAT 6081
- K K T P M G F S Y D T R C F D S T V T E S D I R T E E AGGAAAACCC CAATGGGGTT CTCGTATGAT ACCCGCTGCT TTGACTCCAC AGTCACTGAG AGCGACATCC GTACGGAGGA TTCTTTTGGG GTTACCCCAA GAGCATACTA TGGGCGACGA AACTGAGGTG TCAGTGACTC TCGCTGTAGG CATGCCTCCT 6161
- A I Y Q C C D L D P Q A R V A I K S L T E R L Y V G GGCAATCTAC CAATGTIGTG ACCTCGACCC CCAAGCCCGC GTGGCCATCA AGTCCCTCAC CGAGAGGCTT TATGTTGGGG CCGTTAGATG GTTACAACAC TGGAGCTGGG GGTTCGGGCG CACCGGTAGT TCAGGGAGTG GCTCTCCGAA ATACAACCCC 6241
- G P L T N S R G E N C G Y R R C R A S G V L T T S C G GCCCTCTTAC CAATTCAAGG GGGGAAACT GCGGCTATCG CAGGTGCCGC GCGAGCGGCG TACTGACAAC TAGCTGTGGT CGGGAGAATG GTTAAGTTCC CCCCTCTTGA CGCCGATAGC GTCCACGGCG CGCTCGCCGC ATGACTGTTG ATCGACACCA 6321

721	GCCTGGCATT CGGACCGTAA	TACGGGTCAT	CATGACCTTA GTACTGGAAT	CGGGACTTC GCCCTGAAAG	CCTACTTGGCA AG GATGAACCGT	GTACATCTAC CATGTAGATG	GTATTAGTCA TCGCTATTAC CATAATCAGT AGCGATAATG	TCGCTATTAC AGCGATAATG
801	CATGGTGATG GTACCACTAC	CATGGTGATG CGGTTTTGGC GTACCACTAC GCCAAAACCG	AGTACACCAA TCATGTGGTT	TGGGCGTGGA	TAGCGGTTTG	ACTCACGGGG TGAGTGCCCC	ATTTCCAAGT TAAAGGTTCA	CTCCACCCCA
881	TTGACGTCAA AACTGCAGTT	TTGACGTCAA TGGGAGTTTG AACTGCAGTT ACCCTCAAAC	TTTTGGCACC AAAACCGTGG	AAAATCAACG TTTTAGTTGC	GGACTITCCA AAATGICGTA CCTGAAAGGI ITTACAGCAI	AAATGTCGTA TTTACAGCAT	ATAACCCCGC TATTGGGGCG	CCCGTTGACG
961	CAAATGGGCG GTAGGCGTC GTTTACCCGC CATCCGCAC	GTAGGCGTGT CATCCGCACA	ACGGTGGGAG TGCCACCCTC	GTCTATATAA CAGATATATT	GCAGAGCTCG CGTCTCGAGC	TTTAGTGAAC AAATCACTTG	CGTCAGATCG GCAGTCTAGC	CCTGGAGACG
1041	CCATCCACGC GGTAGGTGCG	CCATCCACGC TGTTTTGACC GGTAGGTGCG ACAAAACTGG	TCCATAGAAG AGGTATCTTC	ACACCGGGAC TGTGGCCCTG	CGATCCAGCC TCCGCGGCCG		GGAACGGTGC	ATTGGAACGC
1121	GGATTCCCCG TGCCAAGAG CCTAAGGGGC ACGGTTCTC	TGCCAAGAGT ACGGTTCTCA	GACGTAAGTA CTGCATTCAT	CCGCCTATAG ACTCTATAGG GGCGGATATC TGAGATATCC	1	CACACCCCTT	TGGCTCTTAT (GCATGCTATA
1201	CTGTTTTTGG GACAAAAACC	CTTGGGGCCT	ATACACCCC TATGTGGGGG	GCTCCTTATG	CTATAGGTGA	TGGTATAGCT A	TAGCCTATAG (ATCGGATATC)	GTGTGGGTTA
1281	TTGACCATTA AACTGGTAAT	TTGACCACTC	CCCTATTGGT	GACGATACTT	TCCATTACTA	ATCCATAACA TAGGTATGT	TGGCTCTTTG C	CCACAACTAT
1361	CTCTATTGGC TATATGCCAA GAGATAACCG ATATACGGTT		TACTCTGTCC :	TTCAGAGACT AAGTCTCTGA	GACACGGACT	CTGTATTTT #	ACAGGATGGG G TGTCCTACCC C	GTCCATTTAT

FIG. 3-Page 2

	TCGCGCGTTT		GGTGAAAACC		CTGACACAT	TCTGACACAT GCAGCTCCCG AGACTGTGTA CGTCGAGGGC	GCAGCTCCCG	GCAGCTCCCG
81 GC	GCCGGGAGCA	GACAAGCCCG	TCAGGGCGCG	TCAGCGGGTG AGTCGCCCAC	3TG		STG TTGGCGGGTG TCGGGGCTGG	TTGGCGGGTG AACCGCCCAC
161 GC	GCAGATTGTA	CTGAGAGTGC GACTCTCACG	ACCATATGAA TGGTATACTT	GCTTTTGCA	سا ہے		StuI A AAAGCCTAGG CCTCCAAAAA F TTTCGGATCC GGAGGTTTTT	
241 AA)	AATAGCTCAG TTATCGAGTC	AATAGCTCAG AGGCCGAGGC TTATCGAGTC TCCGGCTCCG	GGCCTCGGCC CCGGAGCCGG	TCTGCATAAA AGACGTATTT		TAAAAAAAT TATTTTTTA	i .	TAAAAAAAT ATTTTTTA
321 ACT TGA	ACTGGGGGG TGACCCGCCC	GAGGGAATTA CTCCCTTAAT	TTGGCTATTG AACCGATAAC	GCCATTGCAT CGGTAACGTA	1	ACGTTGTATC TGCAACATAG	ACGTTGTATC TATATCATAA TGCAACATAG ATATAGTATT	
401 CAT	CATGTCCAAT GTACAGGTTA	ATGACCGCCA TACTGGCGGT	TGTTGACATT ACAACTGTAA	GATTATTGAC CTAATAACTG	1	TAGTTATTAA ATCAATAATT	TAGTAATCAA ATCATTAGTT	ľ
481 AGC TCG	AGCCCATATA TCGGGTATAT	TGGAGTTCCG ACCTCAAGGC	CGTTACATAA GCAATGTATT	CTTACGGTAA GAATGCCATT	1 4 5	ATGGCCCGCC TACCGGGCGG	TGGCTGACCG ACCGACTGGC	1
561 GAC CTG	GACGTCAATA CTGCAGTTAT	ATGACGTATG TACTGCATAC	TTCCCATAGT AAGGGTATCA	AACGCCAATA TTGCGGTTAT	1 00	GGGACTTTCC	ATTGACGTCA TAACTGCAGT	1 .
641 AAA TTT	AAACTGCCCA ITTGACGGGT	AAACTGCCCA CTTGGCAGTA TTTGACGGGT GAACCGTCAT	CATCAAGTGT GTAGTTCACA	ATCATATGCC TAGTATACGG	∢⊢	AAGTCCGCCC TTCAGGCGGG	CCTATTGACG GGATAACTGC	1

FIG. 3-Page 1

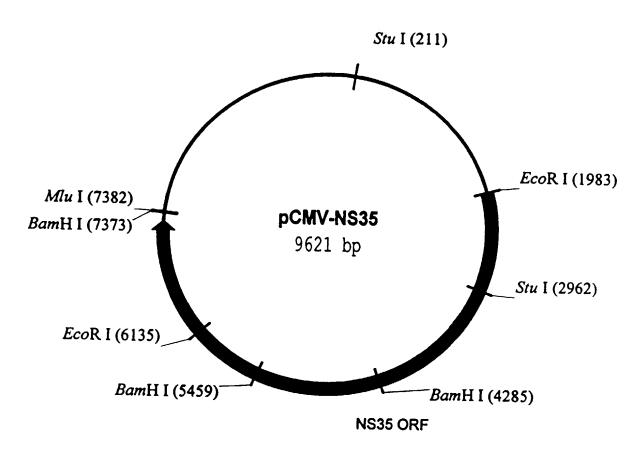


FIG. 2

Cloning Scheme for Generating pCMV-NS35

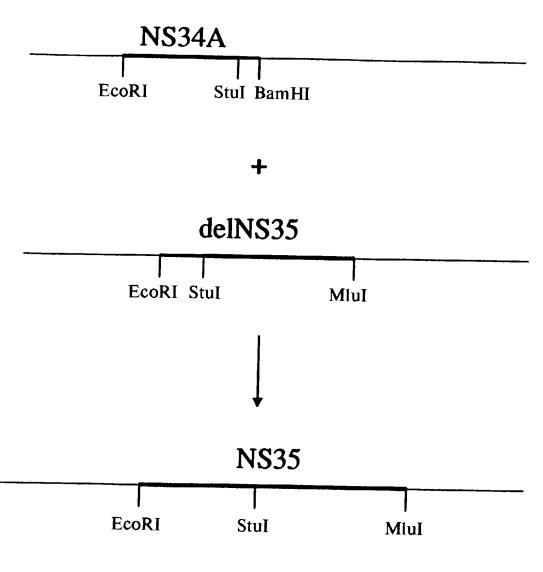


FIG. 1

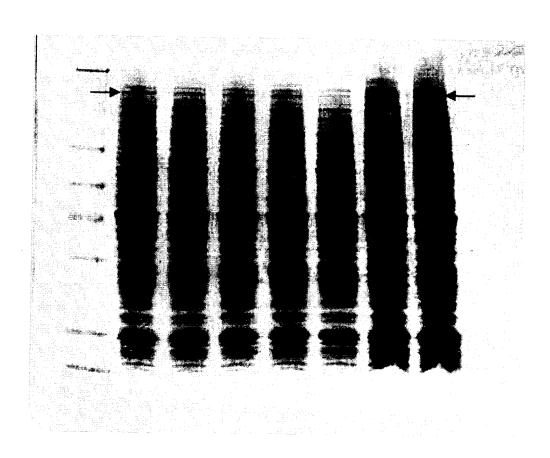


FIG. 23

5449 APAI.

- GlyValArgAlaThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnPro
 5462 GGTGTGCGCGACGAGAAAGACTTCCGAGCGTCGCAACCTCGAGGTAGACGTCAGCCT
 CCACACGCGCGCTGCTCTTCTGAAGGCTCGCAGCGTTGGAGCTCCATCTGCAGTCGGA
 - 5467 BSSH2, 5478 XMNI, 5502 XHOI, 5511 AAT2,
- IleProLysAlaArgArgProGluGlyArgThrTrpAlaGlnProGlyTyrProTrpPro
 5522 ATCCCAAGGCTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGGCCC
 TAGGGGTTCCGAGCAGCCGGGCTCCCGTCCTGGACCCGAGTCGGGCCCATGGGAACCGGG
 - 5548 ALWN1, 5558 ESP1, 5564 SMAI XMAI, 5568 KPNI,
- LeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArg
 5582 CTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCGTGGCTCTCGG
 GAGATACCGTTACTCCCGACGCCCACCCGCCCTACCGAGAGAGGGGCACCGAGAGCC
- ProSerTrpGlyProThrAspProArgArgArgSerArgAsnLeuGlyLysVallleAsp
 5642 CCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTCATCGAT
 GGATCGACCCCGGGGTGTCTGGGGGCCGCATCCAGCGCGTTAAACCCATTCCAGTAGCTA
- ThrLeuThrCysGlyPheAlaAspLeuMetGlyTyrIleProLeuValGlyAlaProLeu
 5702 ACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCCTCTT
 TGGGAATGCACGCCGAAGCGGCTGGAGTACCCCATGTATGGCGAGCAGCCGCGGGGAGAA
 - 5724 HGIE2, 5750 KAS1 NARI, 5756 ECON1,
- GlyGlyAlaAlaArgAlaOC AM

 5762 GGAGGCGCTGCCAGGGCCTAATAGTCGAC
 CCTCCGCGACGGTCCCGGATTATCAGCTG

5650 APAI, 5696 CLAI,

5785 SALI,

FIG. 22-Page 10



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APPL PARTS	NPL	CTNF
MIS A ALAMANA	Non-Patent Literature	Count Non-Final
Internal Misc Paper	OATH	CTRS
LET.	Oath or Declaration	Count Restriction
Misc Incoming Leng (Petition PET.	EXIN
		Examiner Interview
PCT Papers in a 371Application	RETMAIL	M903
· ·	Mail Returned by USPS	DO/EO Acceptance
A Amendment Including Elections	SEQLIST	M905
l =	· · · · · · · · · · · · · · · · · · ·	DO/EO Missing Requirement
Abstract ABST	Specification SPEC	NFDR Formal Drawing Required
		Formal Drawing Required
Application Data Sheet	SPEC NO	NOA
	Specification Not in English	Notice of Allowance
AF/D Affidavit or Exhibit Received	TRNA	PETDEC
	Transmittal New Application	Petition Decision
Appendix APPENDIX		
ARTIFACT		
Artifact	OUTGOING	INCOMING
BIB	CIMS	4B B
Bib Data Sheet	MISC/Office Action	Appeal Brief AP.B
CLM	1449	
Claim	Signed 1449	C.AD Change of Address
COMPUTER	892	_
Computer Program Listing	892	Notice of Appeal
CRFL	ABN	• •
All CRF Papers for Backfile	Abandonment	PA Change in Power of Attorney
DIST	APDEC	
Terminal Disclaimer Filed	Board of Appeals Decision	REM
$_{-}$ DRW $/U$	APEA	Applicant Remarks in Amendment
Drawings	Examiner Answer	XT/
FOR (CTAV	Extension of Time filed separate
Foreign Reference	Count Advisory Action	
FRPR	CTEQ	
Foreign Priority Papers	Count Ex parte Quayle	
IDS	CTFR	
IDS Including 1449	Count Final Rejection	File Wrapper
	· iojoonori	
Internal	ECBOX	FWCLM
ODALT	Evidence Copy Box Identification	File Wrapper Claim
SRNT	WCLM	IIFW
Examiner Search Notes	Claim Worksheet	File Message Indianalisa

WFEE

File Wrapper Search Info

Fee Worksheet

CLMPTO

PTO Prepared Complete Claim Set

FIGURE 1

